Comparative Genomics and Chromosome Evolution in Lepidoptera

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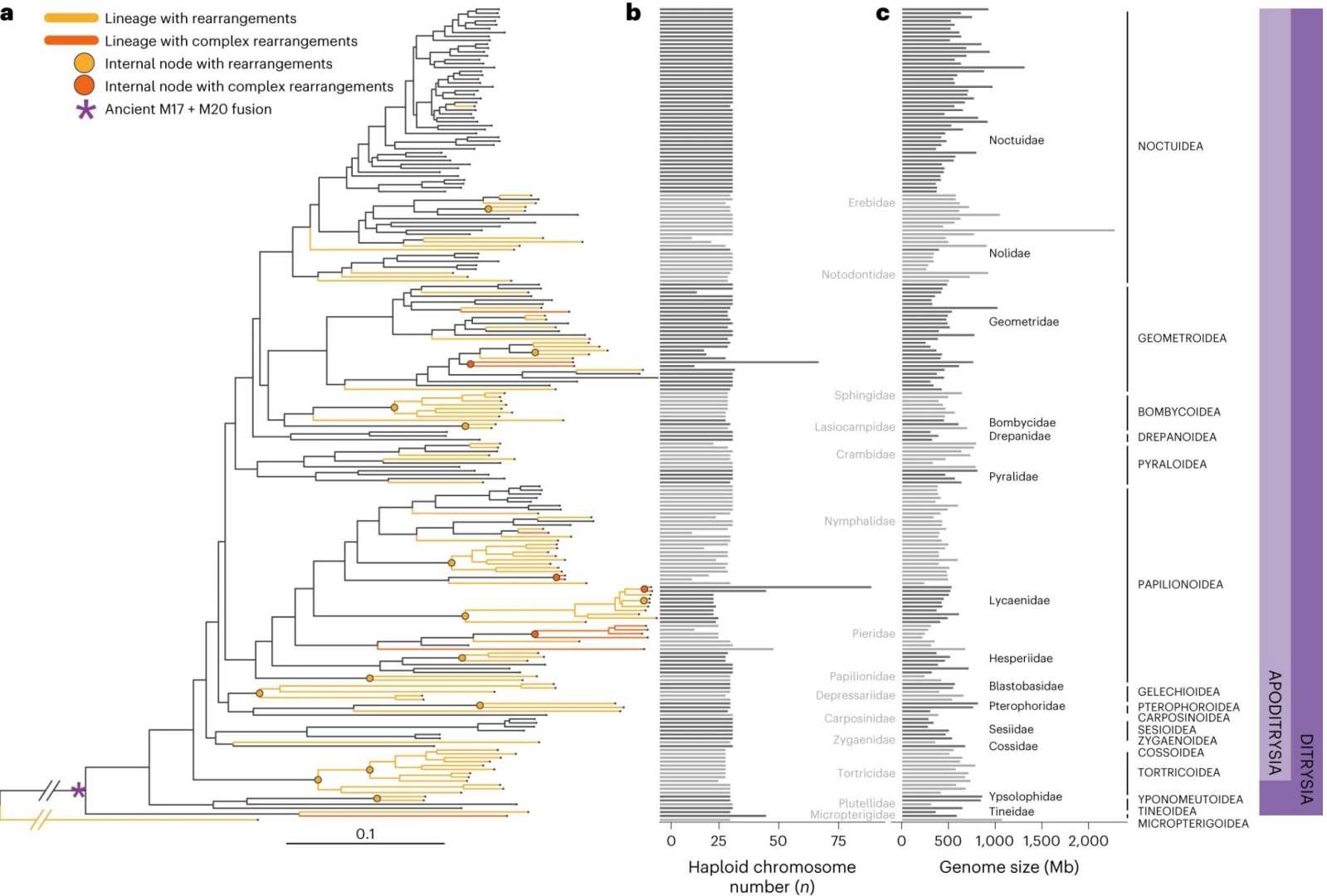
Chromosomal evolution in Lepidoptera (Lepidoptera)

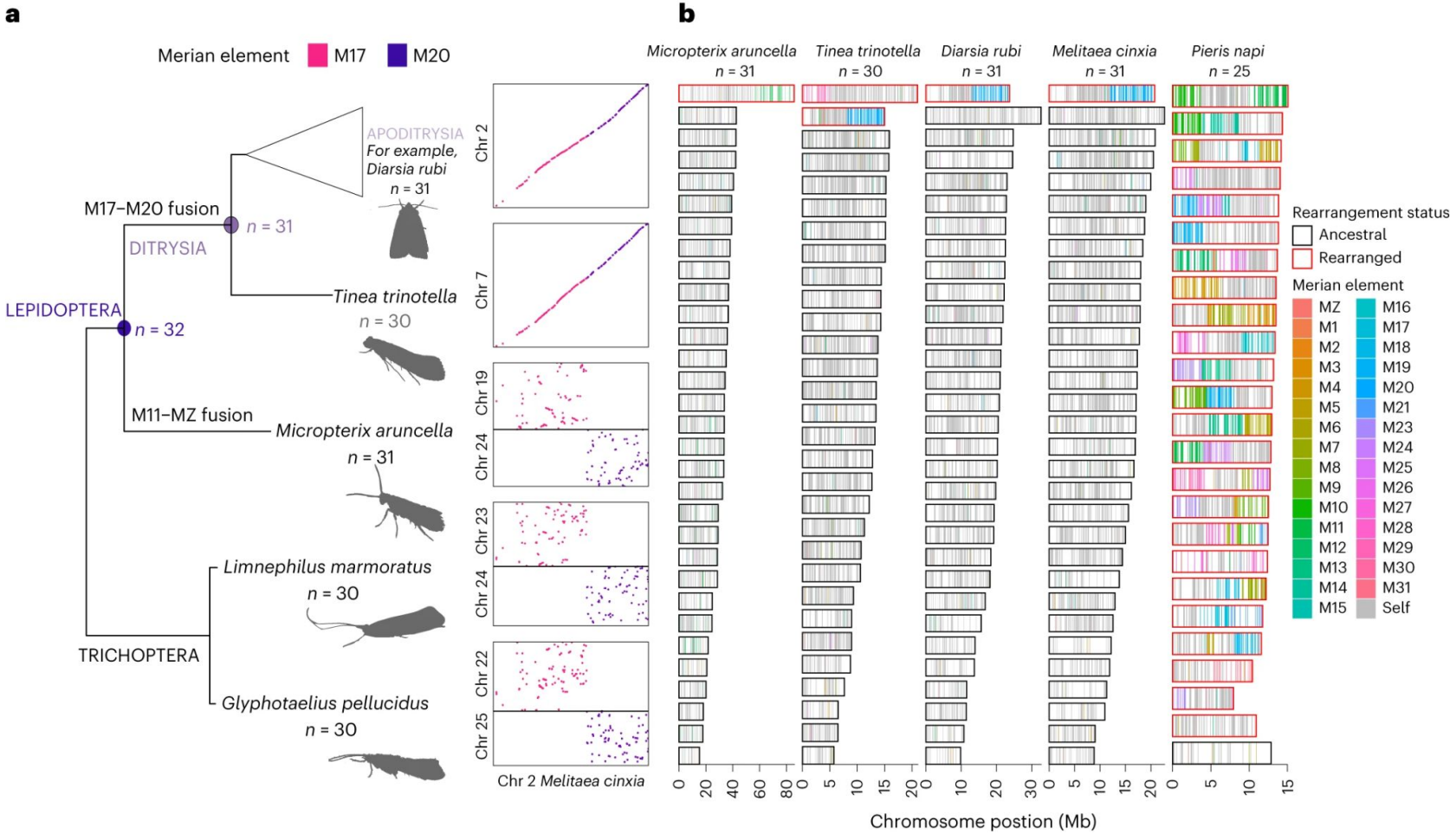
Used **5,287** single-copy orthologues in **210** lepidopteran and **4** trichopteran species to define ALGs in a reference-free, phylogenetically aware manner, using the **tool syngraph**.

4,112 orthologues (78%) were assigned to **32 ALGs.** Hereafter, we refer to these ALGs as Merian elements:

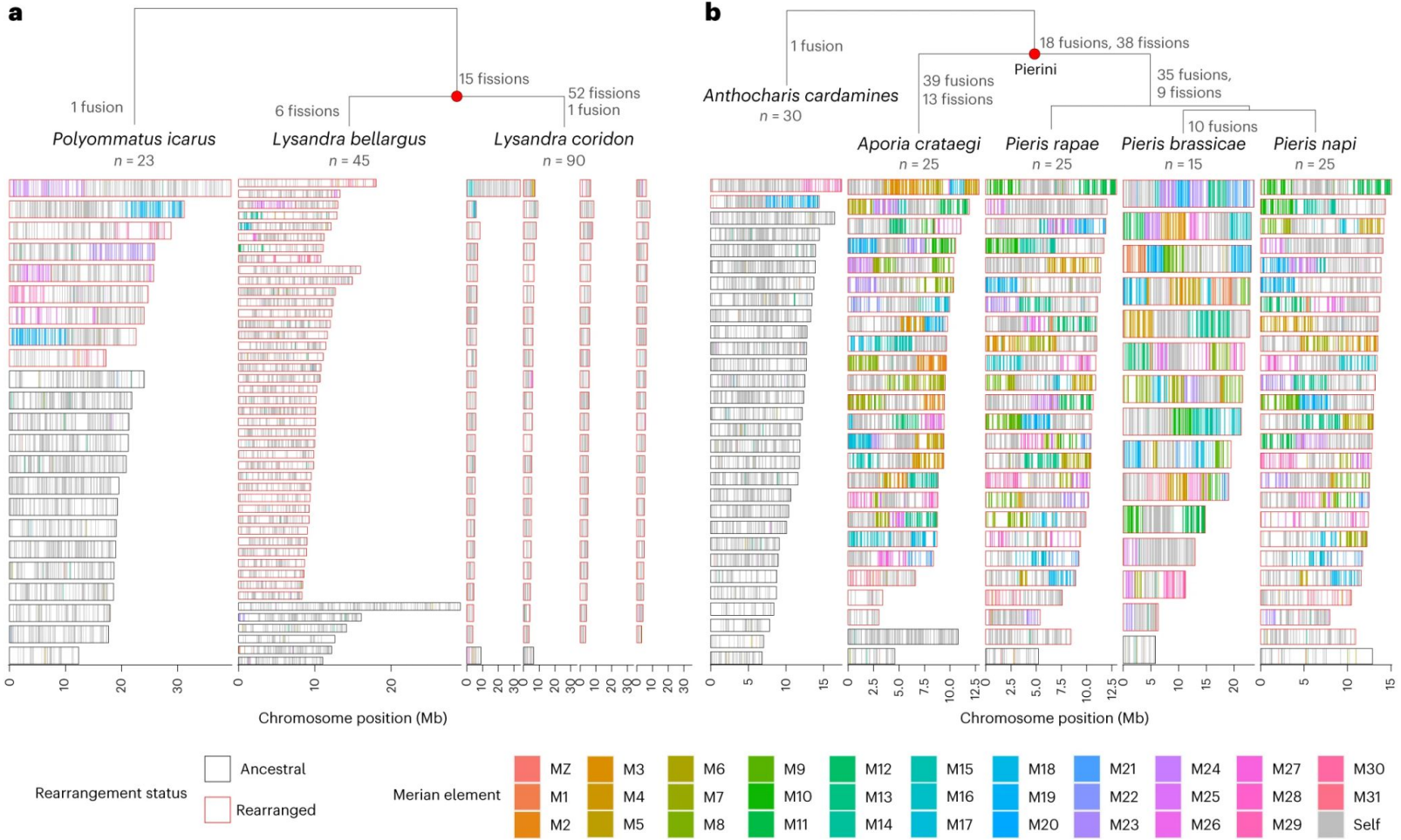
- 31 autosomes and
- Z the sex chromosome



a, Phylogeny was inferred using 4,947 orthologues that were present and single copy in 90% of all species. The tree was rooted using the sister group, Trichoptera (caddisflies).**b ,c,** The distribution of haploid chromosome number (n) and genome size (Mb)



a, Inferred ancestral karyotype of Lepidoptera and the fusion between M17 and M20 found in all Ditrysia. **b**, Merian elements painted across the chromosomes of Micropterix aruncella, Tinea trinotella, Diarsia rubi, Melitaea cinxia and Pieris napi.



a, Relationships of Lysandra species with reorganized genomes and sister species Polyommatus icarus. **b**, Relationships of the Pierini species and their sister species, Anthocharis cardamines, which is not reorganized

Conclusion

- Small as well as sexual Merian elements are more frequently involved in fusion processes.
- Sexual chomosomes were not involved in any of the cases in the rearrangement processes associated with fission.
- Complex rearrangements were observed in 14 species of 8 lineages.
- Although rearrangements are not uncommon in other species with holocentric chromosomes, there have been no other global rearrangements except for the fusion of M17 and M20 elements 200 million years ago (except for some lineages).