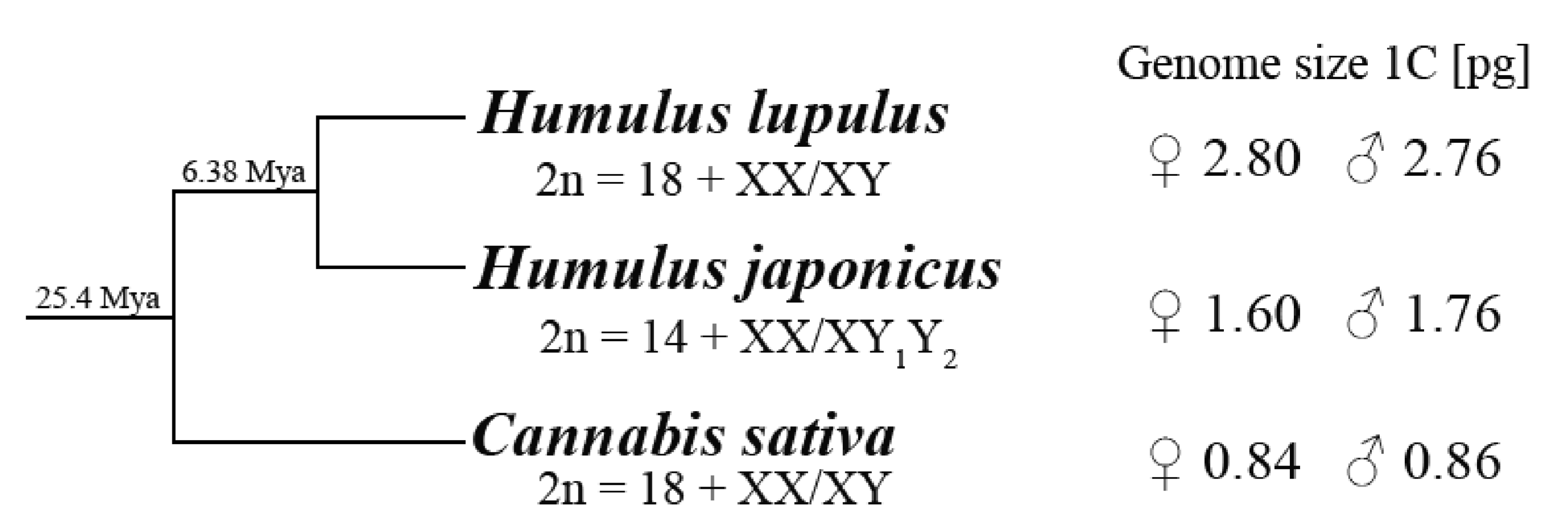


Introduction

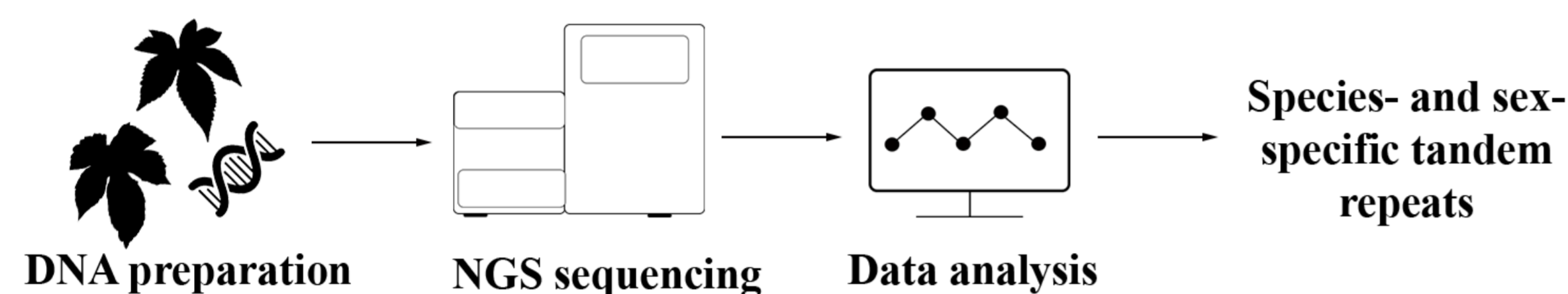
- Humulus lupulus* (common hop) is a perennial and dioecious plant with **XX/XY chromosome system**. Sex chromosomes are heteromorphic – the Y chromosome is smaller compared to X chromosome.
- Related species *Humulus japonicus* and *Cannabis sativa* differ in **genome size, chromosome number, and sex chromosome system**. Nevertheless, it is a unique model for studying the evolution of sex chromosomes.
- Despite hop's importance in the brewing industry evolutionary processes shaping the genomic landscape in the hop are still poorly understood.

The phylogenetic relations in *Cannabaceae* family

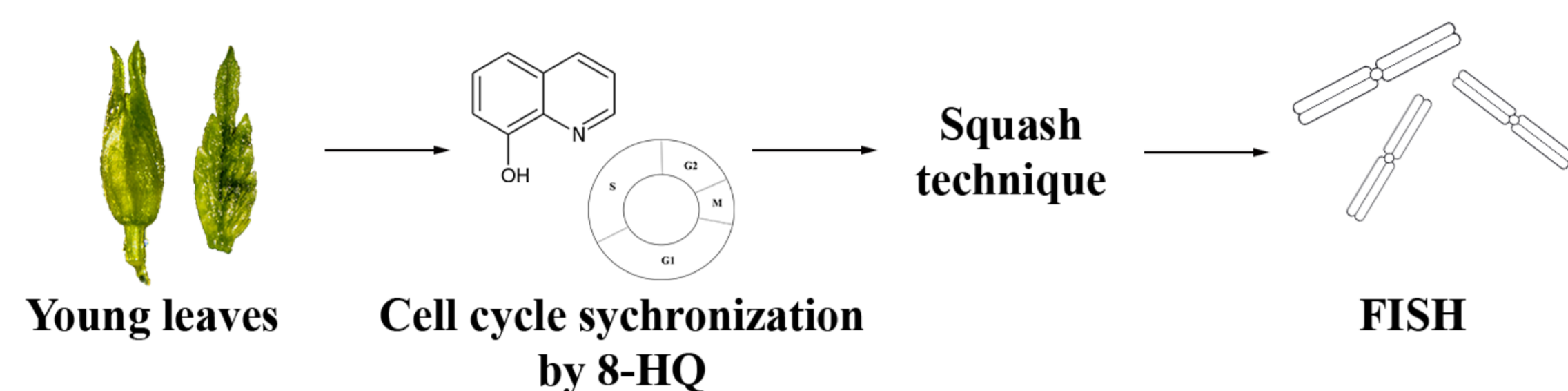


Comparative analysis of *Humulus lupulus* and *Humulus japonicus*

Identification of DNA repeats

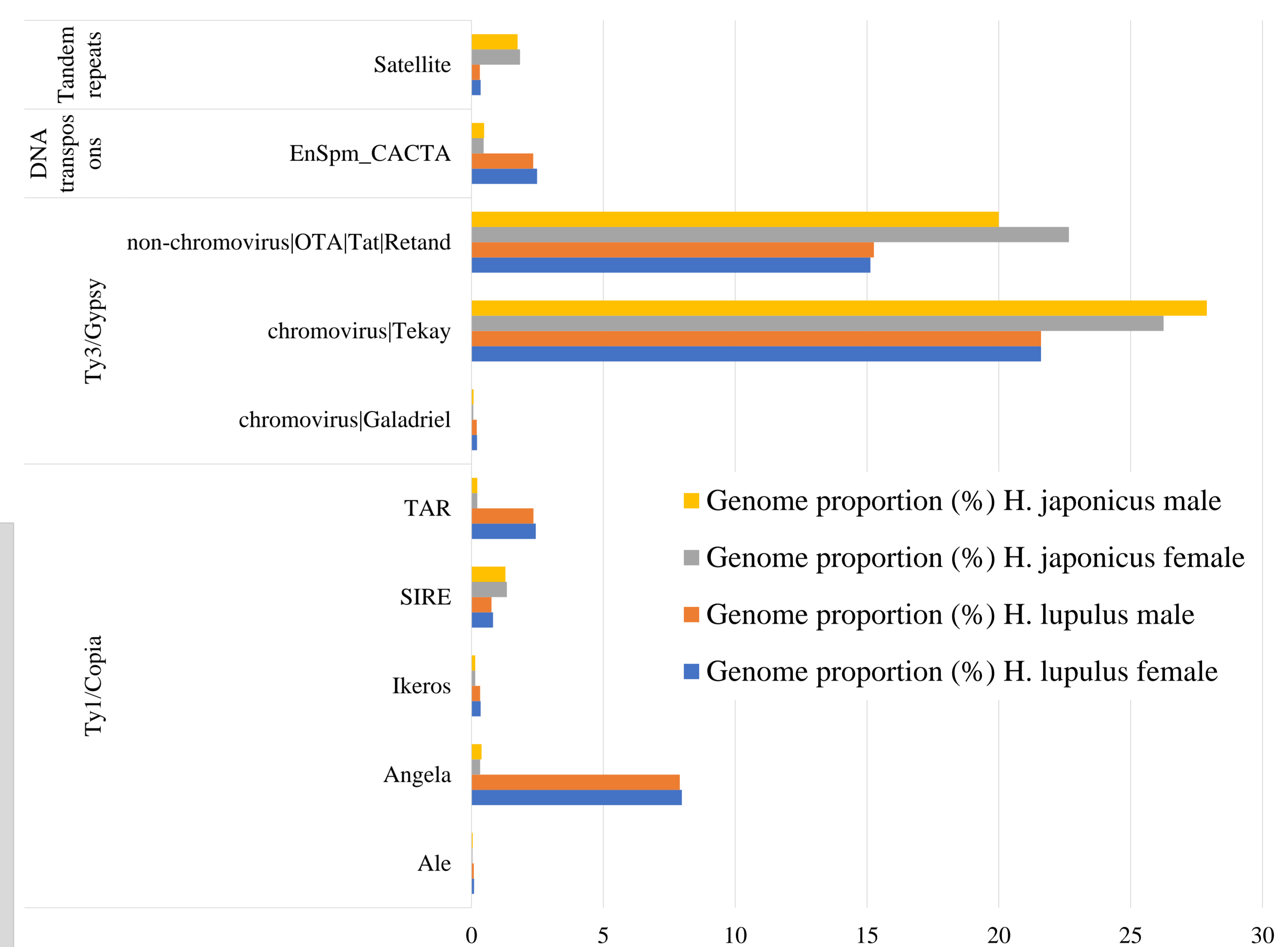


Preparation of *Humulus* metaphase chromosomes



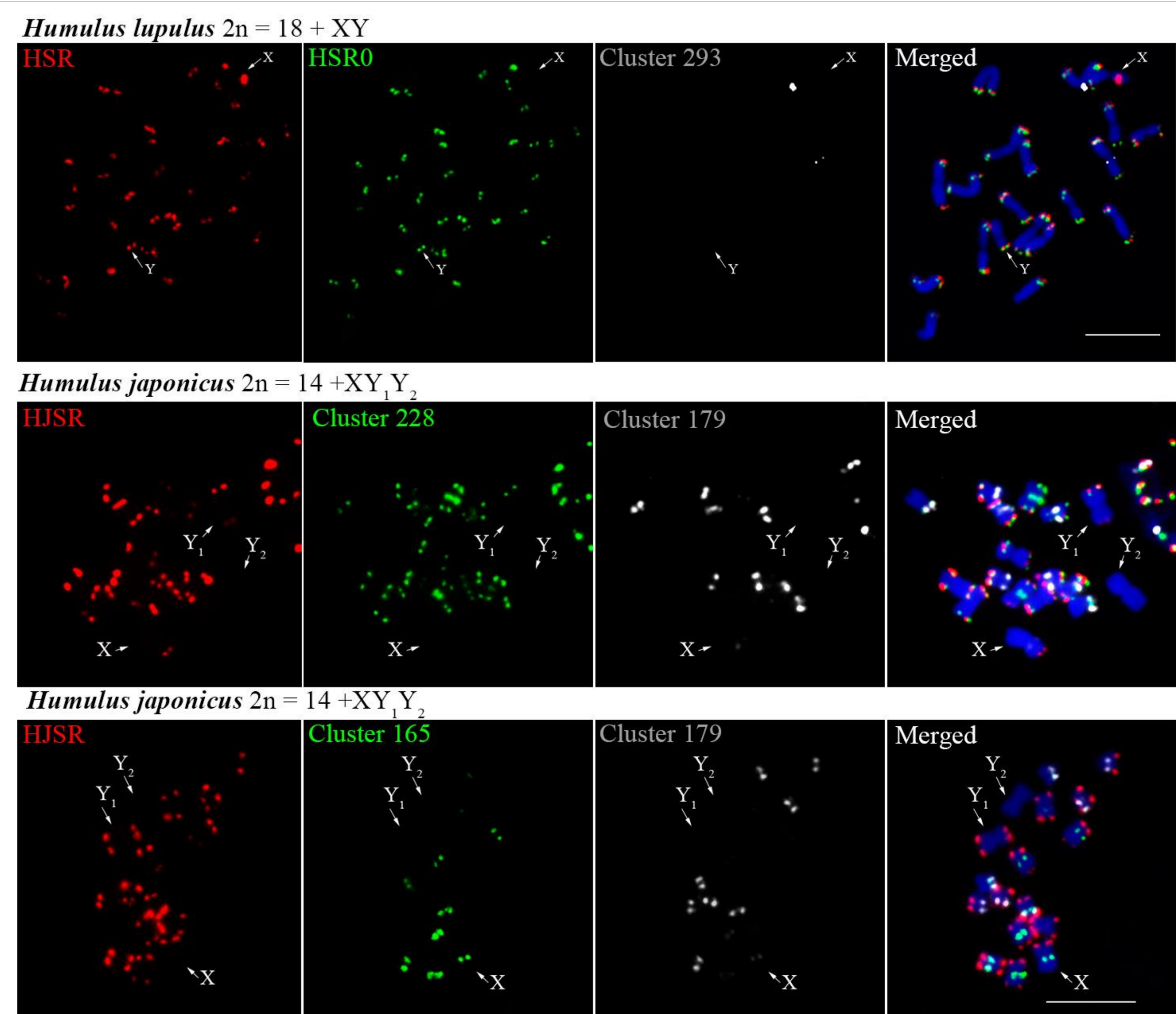
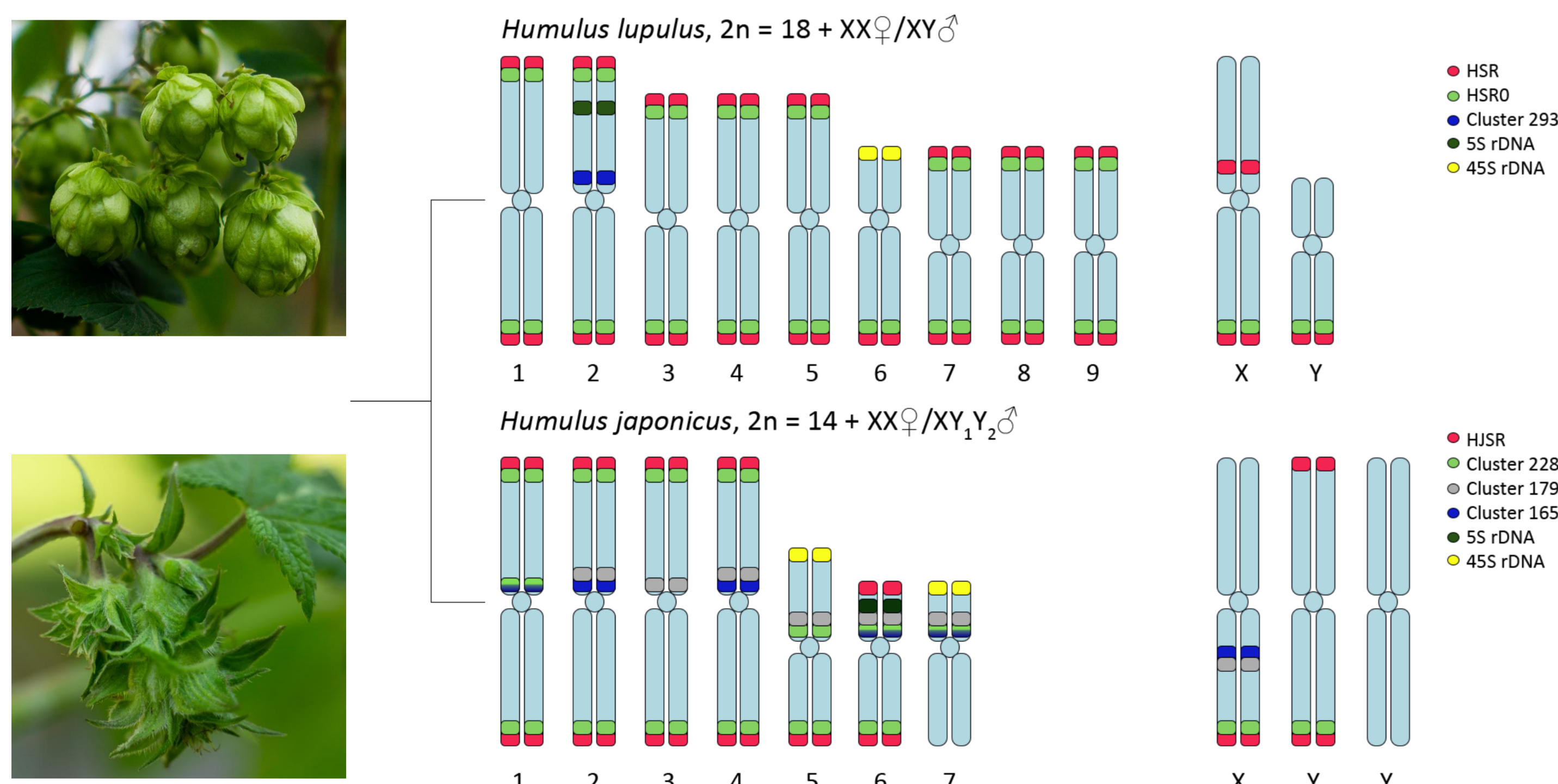
- Repeat composition of the *H. lupulus* and *H. japonicus* genomes were estimated from the genomic abundance of reconstructed contigs using the **RepeatExplorer2** pipeline.
- The proportion of DNA repeats was estimated to be **64.95 %** and **72.66 %** of the *H. lupulus* and the *H. japonicus* genome, respectively.
- Minimal differences** between female and male genomes of both species were observed. **Considerable differences** were found for class of repeats Ty1/Copia (Angela, SIRE, and TAR), Ty3/Copia (Tekay, Athila, and Retand), and tandem repeats (more in the graph).
- This study is focused on the distribution of tandem repeats (satellites) which represent **0.35 %** of the *H. lupulus* genome and **1.80 %** of the *H. japonicus* genome.

Differences in repeat composition between *H. lupulus* or *H. japonicus* female and male genomes



Distribution of tandem repeats on autosomes and sex chromosomes

- Young leaves of *H. lupulus* (Saaz hop) and *H. japonicus* treated by 8-hydroxyquinoline (8-HQ) were used for chromosomes preparation. 8-HQ increases the number of cell in mitosis and allowing to metaphase chromosomes isolation.
- Tandem repeats **HSR¹, HSR⁰, and newly identified cluster cl293** were localized on *H. lupulus* chromosomes (HSR and HSR⁰ in subtelomeric regions and cl293 autosome 2 specific pericentromeric signal).
- Positions of tandem repeats **HJSR³, newly identified clusters cl228, cl179, and cl165** were localized on *H. japonicus* chromosomes (HJSR and cl288 in subtelomeric regions, cl179 and cl165 in pericentromeric regions).
- HSR and HJSR have sequence similarity and have same pattern on metaphase chromosomes. Similar patten were found for HSR⁰ and cluster 228.



Acknowledgment and References

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Conclusion and Future plans

- We identified **new cytogenetic markers (cluster cl293, cl228, cl179, and cl165)** and **localized their position** on autosomes and sex chromosomes.
- Our results suggest the occurrence of **chromosomal rearrangements** during the autosomes and sex chromosome evolution in both species (at least one inversion in *H. lupulus* genome and fusion in *H. japonicus* genome).
- Our findings provide a new tool to study closely related species of the *Cannabaceae* family and their **genome dynamics** in relation of their independent XY evolution.