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# Editorial: Evolutionary cytogenetics of insects

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Editorial on the Research Topic  
[Evolutionary cytogenetics of insects](#)

## Introduction

Modern contributions to evolutionary cytogenetics of insects are aimed at understanding the evolutionary changes of the chromosome structure and function within different taxa and lineages of this enormous group. Various molecular methods, e.g., DNA sequencing, molecular karyotyping, and fluorescence *in situ* hybridization (FISH), are widely used in evolutionary cytogenetic studies in combination with traditional techniques, like chromosome morphometry and conventional bandings, having a synergistic effect on the research. In particular, investigations of the mechanisms and evolutionary roles of chromosomal rearrangements and modifications of meiosis are recently gaining momentum. The origin and evolution of specific features of karyotypes, including sex chromosomes and heterochromatin distribution, are also among the rapidly developing topics. Parallel transformations and reversals are common in the process of insect karyotype evolution, and phylogenetic analysis of the karyotypic change is therefore indispensable. The robust phylogenetic reconstructions are based on independent characters, which often include comprehensive molecular data. All these statements are exemplified by six original papers in this Research Topic.

## Cytogenetic studies of selected species

In-depth studies of selected species by modern cytogenetic techniques provide valuable information on certain features of genome functioning in the living cell. Specifically, [Montiel et al.](#) examined the structure of satellitome, i.e., an array of satellite DNA sequences, in an important pest species, *Rhynchophorus ferrugineus*

Olivier (Coleoptera, Curculionidae). Surprisingly, satellites belonging to 112 families were discovered in this beetle, which represents the most diverse set of this kind among all insects with studied satellitomes. Moreover, these repeats make up approximately 25% of the whole genome of this insect species. FISH with most abundant satellite DNA families showed that all of them were dispersed in the euchromatin, but certain families were also accumulated in the pericentromeric heterochromatic regions. Since about a half of the satellite DNA families were either transcribed throughout the whole ontogenesis or showed stage-specific transcription, the authors speculated about the role of those sequences in the development of *Rh. ferrugineus*.

## Comparative karyotype research

Together with studies of separate species, comparative research of closely related members of certain genera and higher taxa reveals the existing pathways of karyotype polymorphism and evolution in various groups of insects as reported in three published papers. For example, Gouvi et al. compared the structure of mitotic and polytene chromosomes of two important pest species of the genus *Zeugodacus* (Diptera, Tephritidae), *Z. tau* (Walker) and *Z. cucurbitae* (Coquillett) using routine staining and *in situ* hybridization of four molecular markers to the chromosomes of the two species. These approaches allowed identifying karyotypic differences between *Z. cucurbitae* and *Z. tau* as well as chromosomal rearrangements occurred during their evolution. In addition, spatiotemporal dynamics of a particular chromosomal inversion was characterized in details by Sangba Kembi Ngounou et al. in the two Central African malaria vectors, *Anopheles gambiae* Giles and *A. coluzzii* Coetzee et Wilkerson (Diptera, Culicidae), using a PCR-based molecular karyotyping technique. Although frequency of this rearrangement was generally higher in *A. coluzzii*, it neither depended on the local climatic changes in both species nor affected their biting behavior at the microhabitat scale. Finally, Toscani et al. studied distribution of two types of histone modification in six species of true bugs (Hemiptera, Heteroptera). They discovered a form of lysine 9 of histone H3 (H3K9me3) as a universal marker of sex chromosomes from early prophase I to the end of the first meiotic division. Another histone modification, the H3 lysine 9 dimethylation (H3K9me2), also marked the sex chromosomes since early prophase, but showed different dynamics at metaphase I depending on the sex-chromosome segregation. The authors suggested that these histone modifications evolved in Heteroptera as

markers of asynaptic and achiasmatic sex chromosomes during meiosis.

## Phylogenetic reconstruction of karyotype evolution

At a larger phylogenetic scale, evolutionary reconstructions allow to reveal certain pathways of karyotype evolution in various groups of insects. Specifically, Afonso Neto et al. used five nuclear and mitochondrial genes to compose a phylogenetic tree for two trap-jaw ant genera of the subfamily Ponerinae (Hymenoptera, Formicidae), *Anochetus* and *Odontomachus*, and then to reconstruct the evolution of the chromosome number and morphology in these taxa. The authors suggested  $n = 15$  as the ancestral chromosome number of trap-jaw ants. They also identified centric fissions and pericentric inversions as the main rearrangements responsible for the transformations of karyotypes of these two genera. Moreover, inversions apparently led to the changes in the chromosome morphology, whereas fissions changed the chromosome number in *Anochetus* and *Odontomachus*.

## Surveys and databases

Karyotypic information is extensively used in biological research for many years now. However, these data are usually scattered among hundreds of various sources, which, in turn, are often publicly unavailable. Morelli et al. partially solved this problem by compiling two public datasets for the genus *Drosophila* and the order Diptera in general. For example, at the time of creating this paper, the latter interactive database contained about 3,500 karyotype records from more than 500 publications. Synthesizing these data, the authors highlighted several groups of particular interest for future genome sequencing.

## Conclusion

This Research Topic includes original research papers representing a combination of various cytogenetic approaches and different insect taxa. In general, it clearly demonstrates that these studies facilitate our understanding of insect chromosomes and karyotype evolution of this enormous group as well as put forward further perspectives in evolutionary cytogenetics of insects.

## Author contributions

VG wrote a draft version of the paper. All authors contributed to the manuscript and approved its final version.

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