

Coleoptera Karyotype Database

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Source: The Coleopterists Bulletin, 69(1):174-175.

Published By: The Coleopterists Society

DOI: <http://dx.doi.org/10.1649/0010-065X-69.1.174>

URL: <http://www.bioone.org/doi/full/10.1649/0010-065X-69.1.174>

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SCIENTIFIC NOTE

COLEOPTERA KARYOTYPE DATABASE

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Cytogenetic research has a long history in Coleoptera taxonomy and evolutionary biology. The last synthesis of beetle karyotypes was completed in 1978 when only 2,160 beetles had been studied (Smith and Virkki 1978). Since this compilation, the number of beetles that have been targeted by cytogenetic studies has doubled. However, karyotype records are scattered among hundreds of journal articles often with narrow taxonomic or geographic focus. This has made it difficult to analyze large-scale patterns of karyotype evolution across Coleoptera or even determine what data is available for a clade. To eliminate this barrier, we created the Coleoptera karyotype database (www.uta.edu/karyodb/). The database currently contains 4,797 records, but we envision it as a long-term repository that will be regularly updated. This will allow open access to data that were previously scattered and often available only through subscription-based publications.

We store the karyotype data in an SQL database that can be queried using a dynamically updated webpage. Users generate database queries by making selections at up to three taxonomic levels (suborder, family, or genus) and or selections of up to three karyotype characters (sex chromosome system, b-chromosomes, and reproductive mode).

Once a user has defined a query, it is used to produce an html table. The website also allows users to export a comma-separated text file of their results for offline analysis.

The long history of beetle cytogenetics has led to naming conventions that describe not only the number of autosomes and the sex chromosome system but also the behavior of the sex chromosomes during meiosis (Table 1). Testes squashes are the most common method employed in beetle karyotyping, and the karyotypes reported are meioformulas. For example, a commonly reported karyotype is “9+Xy_p” which indicates nine autosomes, an XY sex determination system, and that a small Y chromosome remains at a distance from the X during meiosis. Most organisms require homologous chromosomes to come together and form chiasmata to faithfully segregate the chromosomes into the gametes. However, many beetles, particularly in the suborder Polyphaga, exhibit various forms of distance-pairing sex chromosome segregation of the sex chromosomes.

In addition to variation in sex chromosomes, Coleoptera karyotypes also reveal abundant variation in chromosome number, with diploid number ranging 4–70. Our compilation reveals that variation in chromosome numbers among clades is highly heterogeneous. Some families, such as

Table 1. Common Coleoptera sex chromosome systems (SCS).

SCS	Explanation
XY	The X and Y have some region(s) that recombine during meiosis.
Xy	The X and Y have some region(s) that recombine during meiosis, and the Y is distinctly smaller than the X.
NeoXY	The X and Y have some region(s) that recombine during meiosis, and the sex chromosomes are much larger than closely related species. Authors use this annotation when they believe the sex chromosomes have fused with an autosomal chromosome.
Xyp	The X and Y chromosome do not recombine during meiosis, and instead are distinctly separated from one another (<i>i.e.</i> , distance pairing). The subscript p indicates that the Y chromosome is punctiform and appears suspended from the larger X chromosome during meiosis (similar to a weight hanging from a parachute).
XO	The Y chromosome has been lost and males have an unpaired X.

Scarabaeidae, exhibit remarkably little variation (mean number of autosomes = 8.8 ± 1.0 ; range = 3–17; mode = 9 representing 73% of species). Meanwhile, groups like Chrysomelidae exhibit far greater lability (mean number of autosomes = 11.9 ± 4.16 ; range = 3–31; mode = 11, representing only 16% of species).

Despite our ability to now sequence whole genomes, karyotypes remain valuable sources of data. Karyotypes are a highly variable and complex trait that offers an opportunity to detect changes in genome organization, uncover phylogenetic history, and distinguish cryptic species. Our initial analyses show that using the Coleoptera karyotype data to model sex-chromosome evolution can reveal important insights into the evolution of beetle genomes (Blackmon and Demuth 2014). Additionally, in cases where whole genome sequencing is being done, karyotypes offer a quick and inexpensive form of

preliminary data providing important guidance in choosing species that will be most informative for answering specific biological questions.

While we will continue to update the database with newly published beetle karyotypes, we also welcome direct contributions and corrections. You may contact us or submit data at coelochromosomes@gmail.com.

REFERENCES CITED

- Blackmon, H., and J. P. Demuth. 2014.** Estimating tempo and mode of Y chromosome turnover: explaining Y chromosome loss with the fragile Y hypothesis. *Genetics* 197(2): 561–572.
- Smith, S. G., and N. Virkki. 1978.** *Coleoptera. Animal Cytogenetics Vol. 3 Insecta 5.* Gebrüder Borntraeger, Berlin, Germany.

(Received 23 October 2014; accepted 7 January 2015.
Publication date 18 March 2015.)