

# SPIDERS HAVE GENOMES, TOO!

**T. Ryan Gregory**

Department of Zoology  
University of Guelph  
Guelph, ON  
N1G 2W1  
rgregory@uoguelph.ca

In 1948, Roger and Colette Vendrely observed “a remarkable constancy in the nuclear DNA content of all the cells in all the individuals within a given animal species” [my translation], which they took as evidence that DNA, and not protein, was the hereditary material. In 1951, Alfred Mirsky and Hans Ris reported nuclear DNA contents for a wide variety of animal species. And so began the study of genome size evolution.

Beginning with the survey of Mirsky and Ris, and especially over the decades that followed it, it became apparent that DNA content, constant though it was within species because DNA is the stuff of genes, did not correlate with any intuitive notions of organismal complexity. The question was, How can DNA be what genes are made of, and yet not correlate in amount with the presumed number of genes? Why should it be, for example, that an *Amoeba* has 200 times more DNA than a human? By the early 1970s, this confusing observation had become known as the “C-value paradox”; C-value referring to the haploid, or 1C *class* of DNA, now also called the genome size.

The solution to the “paradox”, of course, is that not all (or even much!) DNA is genes. In fact, the vast majority of the eukaryotic DNA on the planet takes the form of non-coding sequences like extinct gene duplicates (“junk DNA”), transposable elements (“selfish DNA”), repeats of various lengths (e.g., microsatellites), and so on. A big genome, therefore, does not imply a lot of genes. (And, in fact, a complex organism may not imply a lot of genes either, if the recent estimates from the human genome sequence are correct!).

So much for the C-value paradox, but this doesn't mean that the puzzle of genome size evolution has been solved. Several important questions remain, such as Where does all this non-coding DNA come from? Why do some groups have so much of it, and others so little? What impact, if any, does all this genetic baggage have on the organism? Together, these make up what I have called the “C-value enigma”. Obviously, to answer these questions it will be necessary to compare genome sizes and structures across a diverse array of taxa.

Botanists recognized the need to compile genome size information early on. Since 1976, they have been publishing long lists of plant C-values, and as of 1995 this has been available as a searchable online database (<http://www.rbgekew.org.uk/cval/homepage.html>). Zoologists have lagged far behind on this matter, but last year the Animal Genome Size Database came into being (<http://www.genomesize.com>). Both of these resources have enabled broad comparative studies which have revealed some important relationships between genome size and the organismal phenotype (for example, correlations with cell size, developmental rate, metabolism, body size, etc.). They have also exposed major gaps in our current dataset.

Although invertebrates make up the dominant forms of multicellular life on Earth, they are currently represented by only about 900 species in the Animal Genome Size Database (vs. 2100 vertebrates). Some groups are entirely absent notably, not a single spider genome size has ever been published. This, despite the fact that arachnids will almost certainly provide some important insights into the evolution of the genome. (As an example, I recently estimated the genome of the two-spotted spider mite, *Tetranychus urticae*, to be one of the smallest among arthropods at only 0.08pg that is, only about 40% of *Drosophila melanogaster*'s, and even smaller than that of *Caenorhabditis elegans*).

In an effort to rectify this colossal taxonomic neglect, I recently collected spiders from various locations in southern Ontario. In one summer of casual sampling (= hiking around with vials in my pockets), I was able to get genome size estimates for about 300 species. (This is a significant sample given the current shortage of invertebrate genome size data in the world, but it is still less than 1% of described spider species).

For spiders, genome size measurements consist of getting haemolymph onto microscope slides, staining these by the Feulgen reaction, and then measuring stain density with a computerized image analysis system. The verdict is still out on the exact number of species and families included in this study, pending the completion of identifications by my collaborator David Shorthouse. Nevertheless, it appears that spider genome sizes vary by at least an order of magnitude, from about 0.5 to 5.7pg in my collection. (By comparison, the human genome is about 3.5pg; all mammals vary only about four-fold, and birds only two-fold). How this variation is distributed, and whether it is associated with key organismal traits, remains to be assessed.

Interesting patterns of genome size variation in spiders and other invertebrates are beginning to illuminate some of the puzzles that make up the C-value enigma, but so far these remain no more than glimpses. Perhaps most importantly, they indicate that it is time to shed light on groups formerly eclipsed by the shadow of biology's vertebrate bias.

#### *Post script*

This initial survey of Ontario spiders is neither exhaustive nor definitive. Readers interested in contributing samples are encouraged to contact me at [rgregory@genomesize.com](mailto:rgregory@genomesize.com). Straightforward instructions for preparing spider samples on microscope slides are available from the Animal Genome Size Database (<http://www.genomesize.com/instr-spiders.htm>). Sincere thanks to Dave Shorthouse for the offer to contribute this piece, and to Maydianne Andrade for providing samples of haemolymph from various *Latrodectus* species.

## RECENT CANADIAN ARACHNOLOGIST ACTIVITIES

### **BENNETT, ROBB**

Robb is presently involved in:

- 1) BC, Copper River area spiders: effects of various silvicultural scenarios (with Staffan Lindgren, UNBC)
- 2) Distribution of *Tegenaria agrestis* and *T. duellica* in BC and NW USA (with Rick Vetter, UC, Riverside)
- 3) Life History and interaction of *T. agrestis* and *T. duellica* at a beach site on Vancouver Island (with Jesse Senecal and Richard Ring, UVic)
- 4) Taxonomy of introduced *Tegenaria* spp. in BC and NW USA
- 5) Taxonomy of *Gnaphosa snohomish*
- 6) The Spiders of British Columbia (with Dave Blades (Royal BC Museum), Don Buckle, Rick West, and Charlie Dondale)
- 7) Ontogeny of female genitalia in species of *Cybaeus* spiders
- 8) Taxonomy and natural history of North American cybaeid spiders
- 9) Curation of dictynoid/amaurobioid spiders at CNC, Ottawa
- 10) Attempting to develop a RATIONAL approach to working spiders and other inverts into species-at-risk recovery planning

Bennett R. G. 2002. Hyperbole and hysteria along the path to enlightenment OR Show me your genitalia and I'll tell you what species you are OR The brown recluse (*Loxosceles reclusa*) and the hobo spider (*Tegenaria agrestis*) in British Columbia (Araneae: Sicariidae and Agelenidae). Abstract of paper presented at 100th Anniversary Annual General Meeting of the Entomological Society of BC. *Boreus* **21(2)**:16.

Bennett, R. G. 2001. Spiders (Araneae) and araneology in British Columbia. *Journal of the Entomological Society of British Columbia* **98**:85-92.

Bennett, R. G. 1999. Canadian spider diversity and systematics. *Newsletter of the Biological Survey of Canada (Terrestrial Arthropods)* **18(1)**:16-27.