

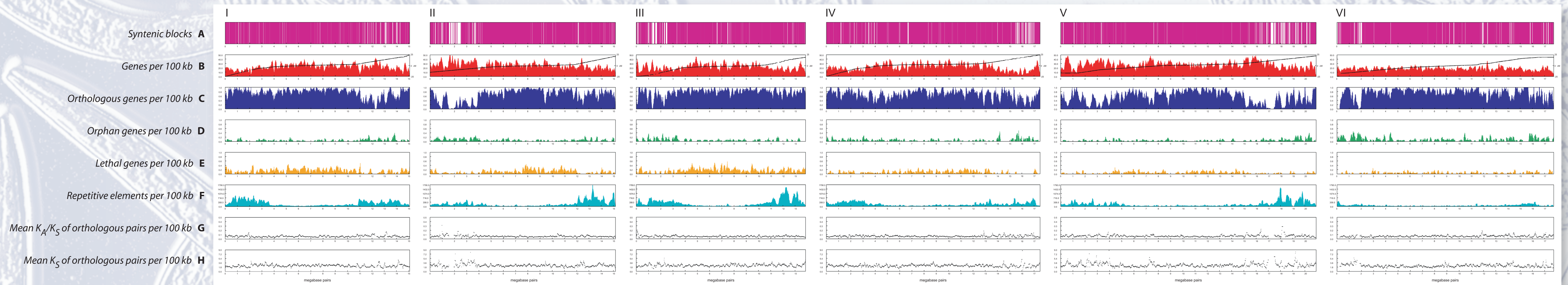
The Genome Sequence of *Caenorhabditis briggsae*: A Platform for Comparative Genomics

The nematodes *Caenorhabditis briggsae* and *Caenorhabditis elegans* diverged 80–110 million years ago, near to the time of divergence of human from mouse, but the nematodes are almost indistinguishable morphologically, have a very similar genome size, and occupy the same ecological niche. To explore the basis of this morphological and functional conservation, the genome sequence of *C. briggsae* has now been determined to a high quality draft stage and compared with that of *C. elegans*. These figures demonstrate the high degree of morphological similarity between *C. briggsae* and *C. elegans* and show how the patterns of evolutionary conservation between the two species vary across the five autosomes (I–V) and sex chromosome (X) of *C. elegans*.

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Each panel corresponds to a *C. elegans* chromosome, and the individual tracks show different measurements of evolutionary divergence:

Track A Regions of synteny (colinearity) between *C. elegans* and *C. briggsae*. White areas correspond to areas where the two genomes could not be aligned due to divergence, and are more abundant in the chromosome arms.

Track B *C. elegans* gene density and genetic map position. Gene density is plotted as a histogram, showing a relatively uniform distribution of genes across each chromosome. The relationship of the position of genes on the genetic map to their position on the sequence is superimposed on the Y axis. Steeper slopes in this plot indicate higher rates of meiotic recombination. Inflection points in the genetic map plot reflect the division of the chromosomes into recombinationally active "arms" and recombinationally slow "centers."

Track C *C. elegans/C. briggsae* orthologs normalized for gene density in 100 kbp sliding windows. Prominent regions of low ortholog density are seen on chromosome arms.

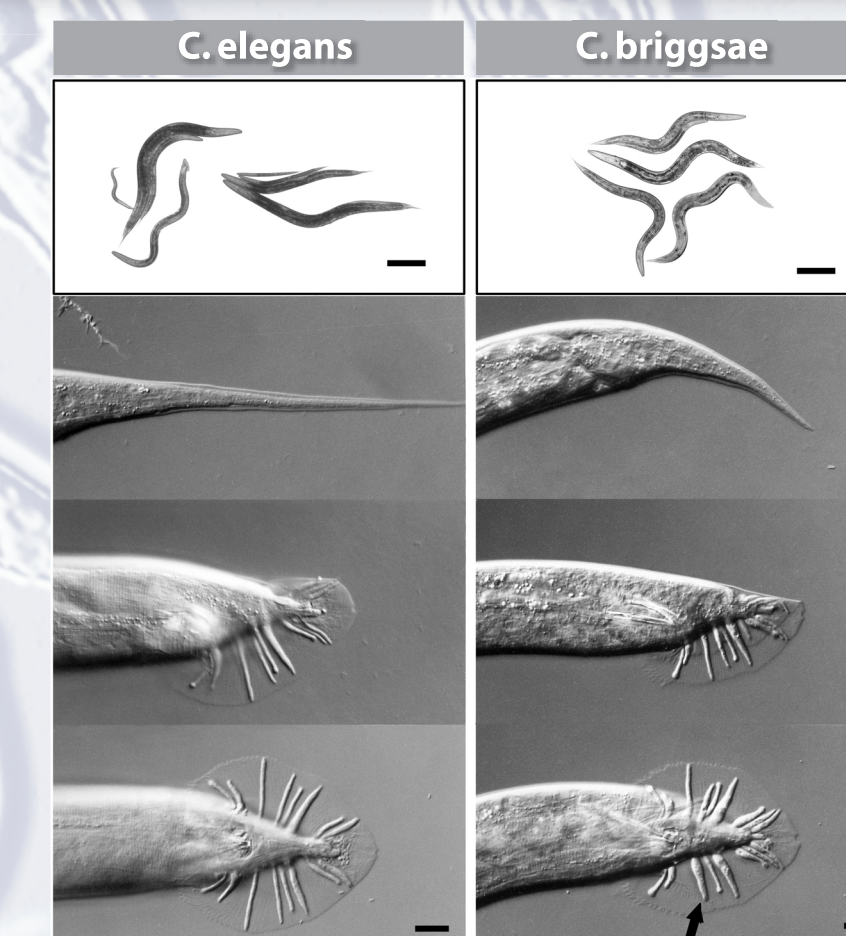
Track D *C. elegans* "orphans," genes with no significant protein similarity in *C. briggsae* or the non-*C. elegans* portion of SwissProt. This histogram has been normalized for gene density in 100 kbp sliding windows. Spikes in orphan density seem to correlate with regions of low-ortholog density.

Track E *C. elegans* genes that mutate to lethality or are lethal in RNAi screens, in 100 kbp sliding windows normalized to overall gene density. This track shows the distribution of essential genes and demonstrates their tendency to cluster in the chromosome centers.

Track F Repetitive elements, binned in 100 kbp sliding windows. Repeat-rich regions correlate with both the absence of significant syntenic coverage and ortholog-poor regions.

Track G The mean ratio of non-synonymous amino acid substitutions to synonymous amino acid substitutions (K_A/K_S) in ortholog pairs in 100 kbp sliding windows. Lower values indicate greater levels of purifying selection.

Track H The mean rate of synonymous amino acid substitutions (K_S) within ortholog pairs, in 100 kbp sliding windows.



Shown are photomicrographs of *C. elegans* (strain CB4088; left panels) and *C. briggsae* (strain PB102; right panels). Depicted from top to bottom for each species are low-magnification, polarized-light images of whole worms (top panels; bar is 200 μ m), higher magnification Nomarski DIC images of female (hermaphrodite) tails, and left lateral and ventral views of male tails (bottom panels; bar is 10 μ m). The arrow in the lower right panel indicates an instance of the fairly frequent fusion of rays 3 and 4 in this strain of *C. briggsae*, one of the morphological features used to distinguish the two species (from Fitch and Emmons 1995).

Fitch DHA, Emmons SW (1995) Variable cell positions and cell contacts underlie morphological evolution of the rays in the male tails of nematodes related to *Caenorhabditis elegans*. *Dev Biol* 170: 564–582.