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The chromosomes of the Filariae

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Abstract

An understanding of the nature of the chromosomes of the filariae is expected to greatly assist the future interpretation of genome data. Filarial development is not eutelic, and there does not seem to be a fixed number of cell divisions in the way that there is in *Caenorhabditis*. It is not clear whether the chromosomes of the filariae have localized centromeres or whether they are holocentric. Sex determination is by a chromosomal "balance" X0 system in most filariae, but in some Onchocercidae there has been a chromosomal fusion to create a neo-XY system. It is presumed that the molecular basis of sex determination in filariae is similar to *Caenorhabditis*. The ancestral karyotype of the filariae is probably 5A+X0, but in some Onchocercidae this has been reduced to 4A+XY, and in *O. volvulus* and *O. gibsoni* it has been further reduced to 3A+XY. *Onchocerca volvulus* and *O. gibsoni* both have supernumary (B-) chromosomes and in *O. volvulus* there is a single active nucleolus organising region near the middle of the long autosome.

Background

Filariae and other nematodes have small genomes relative to other multicellular eukaryotes. Onchocerca volvulus and Wuchereria bancrofti have estimated haploid genomes of 1.5 and 0.81 × 108 nucleotide pairs respectively [1], and this corresponds, for example, to genome sizes of 30 and 2.78×10^8 in humans and Anopheles gambiae respectively [2]. Because of the small genome size, the chromosomes of the filariae are correspondingly small. This makes it difficult to see their gross morphological features, which are at the limits of resolution of the light microscope, and consequently the cytogenetics of the Filariae have not been well studied. However, the physical structure of the chromosomes is a reflection of the organisation of the DNA and its genetics. For example, the chromosomes determine the number of linkage groups and the pattern of sex linkage, and how this can vary between species. The interpretation of the available nuclear genome sequence of *Brugia malayi* and the expressed sequence tag (EST) libraries for *Onchocerca volvulus*, *Onchocerca ochengi*, *Wuchereria bancrofti*, *Brugia malayi*, *Dirofilaria immitis* and *Litomosoides sigmodontis* [3] as well as any possible *O. volvulus* genome sequencing project will be helped by an understanding of their chromosomes.

Eutely, centromeres and sex determination

The observations of Goldschmidt [4] established the idea that postembryonic growth in nematodes occurred without further cell division, and this became known as eutely. For more than 70 years this idea became established in the general literature (for example, [5]), but it is now clear that there are many species where it is not true. For example in *Caenorhabditis elegans* there is a 1.47-fold increase in the number of somatic nucleii [6] and in *Romanomermis culicivorax* there is an 8-fold increase during the parasitic phase [7]. However, these two species contrast another