

# The Genome of *Caenorhabditis bovis*

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## SUMMARY

The free-living nematode *Caenorhabditis elegans* is a key laboratory model for metazoan biology. *C. elegans* has also become a model for parasitic nematodes despite being only distantly related to most parasitic species. All of the ~65 *Caenorhabditis* species currently in culture are free-living, with most having been isolated from decaying plant or fungal matter. *Caenorhabditis bovis* is a particularly unusual species that has been isolated several times from the inflamed ears of Zebu cattle in Eastern Africa, where it is associated with the disease bovine parasitic otitis. *C. bovis* is therefore of particular interest to researchers interested in the evolution of nematode parasitism. However, as *C. bovis* is not in laboratory culture, it remains little studied. Here, by sampling livestock markets and slaughterhouses in Western Kenya, we successfully reisolated *C. bovis* from the ear of adult female Zebu. We sequenced the genome of *C. bovis* using the Oxford Nanopore MinION platform in a nearby field laboratory and used the data to generate a chromosome-scale draft genome sequence. We exploited this draft genome sequence to reconstruct the phylogenetic relationships of *C. bovis* to other *Caenorhabditis* species and reveal the changes in genome size and content that have occurred during its evolution. We also identified expansions in several gene families that have been implicated in parasitism in other nematode species. The high-quality draft genome and our analyses thereof represent a significant advancement in our understanding of this unusual *Caenorhabditis* species.

## INTRODUCTION

The free-living nematode *Caenorhabditis elegans* is used extensively as a model for animal development, genetics, and neurobiology. As the most well-studied species within the phylum Nematoda, *C. elegans* has also become a model for this extremely abundant and diverse group of animals, many of which are parasites [1, 2]. Attempts to understand the evolutionary origins and genetic basis of nematode parasitism often involve comparisons between parasitic nematode species and *C. elegans* [3, 4]. However, *C. elegans* is only distantly related to most parasitic species, which limits the efficacy of comparative studies [1]. Recent years have seen significant progress in our understanding of *Caenorhabditis* diversity, with over 30 new species discovered in the last decade [5–8]. However, all of the ~65 species currently in culture are free-living, with the vast majority having been isolated from rotting fruits and flowers [5–8].

*Caenorhabditis bovis* [9] is therefore particularly unusual for a *Caenorhabditis* species, having been isolated several times from the outer auditory canals of Zebu cattle in Eastern Africa [10] and recently from Gyr cattle in South America [11]. *C. bovis* is believed to be the causative agent of bovine parasitic otitis, a disease that causes a range of symptoms including inflammation, dark brown discharge from the affected ear, and dullness [12]. In severe cases, bovine parasitic otitis can result in mortality [12]. As is typical for a *Caenorhabditis* species, *C. bovis* is believed to have a phoretic association with an invertebrate, with larvae of the Old World screwworm fly (*Chrysomya bezziana*) also being found in the ears of Zebu cattle [12, 13]. It is unclear to what extent bovine parasitic otitis is caused directly by *C. bovis* or by bacterial and/or fungal infections, and therefore to what extent *C. bovis* can be considered a parasite. Despite this, its close association with a vertebrate means that *C. bovis* is of particular interest to researchers interested in the evolution of nematode parasitism and in *Caenorhabditis* diversity. However, as *C. bovis* is not in laboratory culture, it remains little studied.

In collaboration with local veterinarians and scientists, we sampled cattle at livestock markets and slaughterhouses in

