

Abstract

Phylogenetics is the inference of evolutionary relationship between species. With advances in sequencing, phylogenomics or inferring species phylogenies using thousands of genes from multiple genomes is considered to be advantageous over conventional approach of only using one or a few marker genes. In nematodes, other than the model *Caenorhabditis elegans*, most species with genome sequence available are mostly parasites for their impacts on animal health and agricultural productivity. In contrast, genome resources of free-living nematodes are limited, especially nematodes in basal lineages. Resolving their evolutionary relationship as well the genes they contain in the genomes of these most abundant animals on earth provide an opportunity to understand their origin, genomic bases of their diversity and evolutionary histories such as transition of parasitism. Hence, in our research, we have focused on trying to isolate and attempts to sequence genomes and the transcriptomes of free-living nematodes from Dorylaimia, Enoplia and early-branching species in Chromadoria. I will present our efforts in attempt to alleviate the challenges of culturing these nematodes by sequencing the genomes and transcriptomes using amplification techniques. By comparing the genome and the transcriptome of the free-living nematodes, we aim to gain insight into the early evolution of the nematodes.

Result

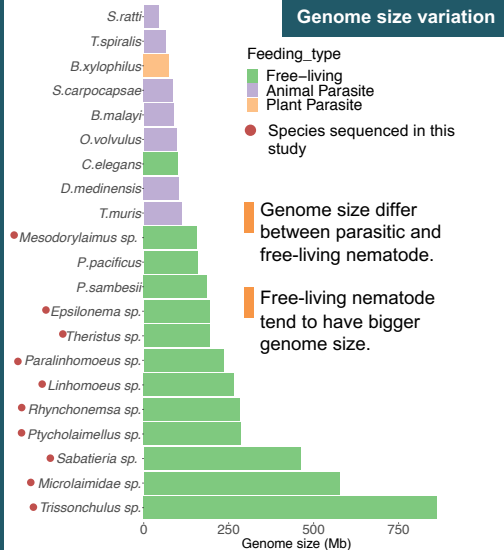
Genome size variation

Feeding_type
■ Free-living
■ Animal Parasite
■ Plant Parasite

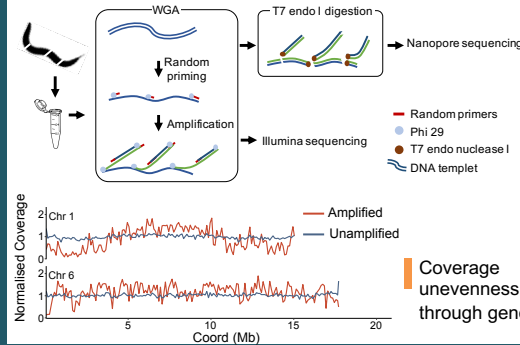
● Species sequenced in this study

Genome size differ between parasitic and free-living nematode.

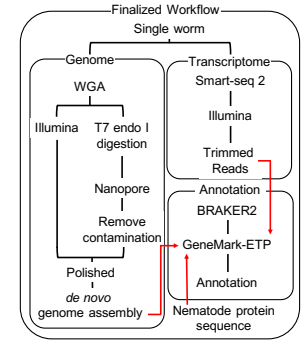
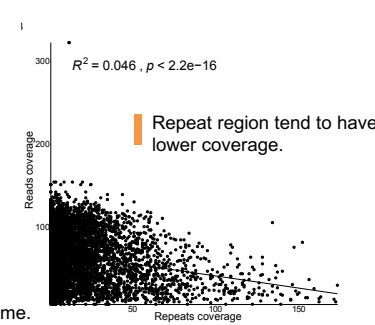
Free-living nematode tend to have bigger genome size.



Method



Coverage unevenness through genome.

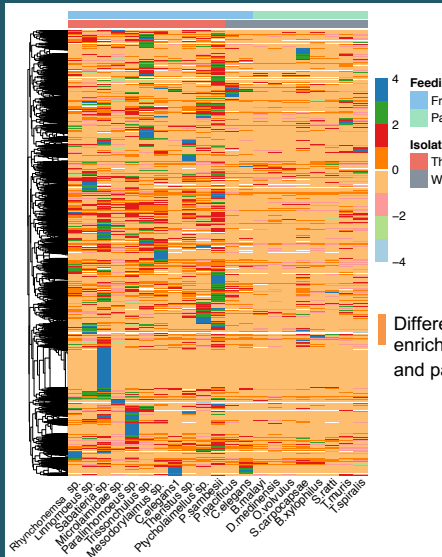


Protein family analysis

Feeding_type
■ Free living
■ Parasite

Isolate
■ This study
■ Wormbase

Different genes are enriched in free-living and parasitic nematodes



Build with 26 orthologs.

More species genome in early-branching lineage are needed.

Phylogenetic Tree

