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A Genome of *Brugia Malayi* Filarial Nematode

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Intro. To genomics (485)



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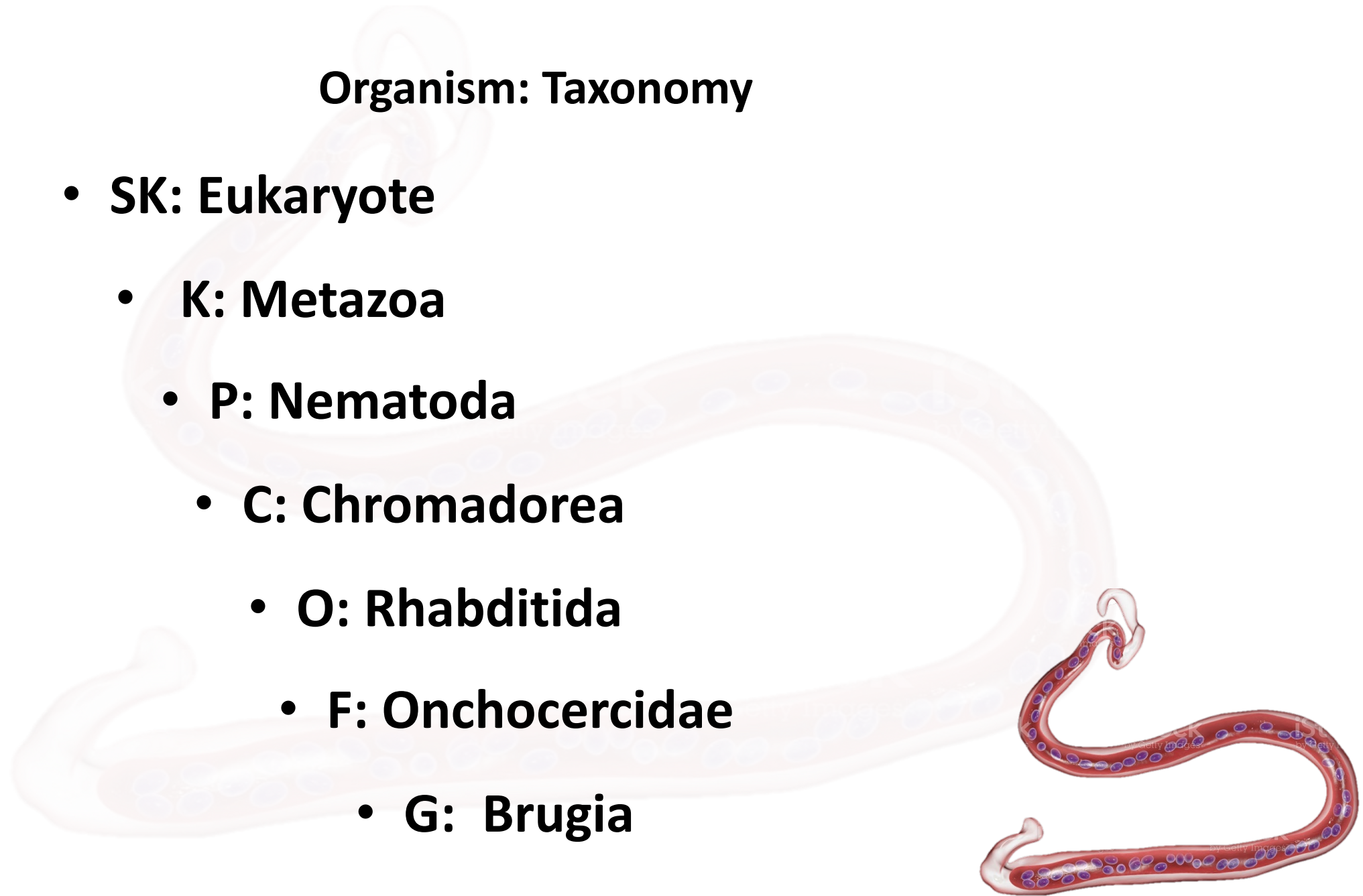
Selected paper

Draft Genome of the Filarial Nematode Parasite *Brugia malayi*

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Organism: Taxonomy

- **SK: Eukaryote**
 - **K: Metazoa**
 - **P: Nematoda**
 - **C: Chromadorea**
 - **O: Rhabditida**
 - **F: Onchocercidae**
 - **G: Brugia**



Physical characteristics

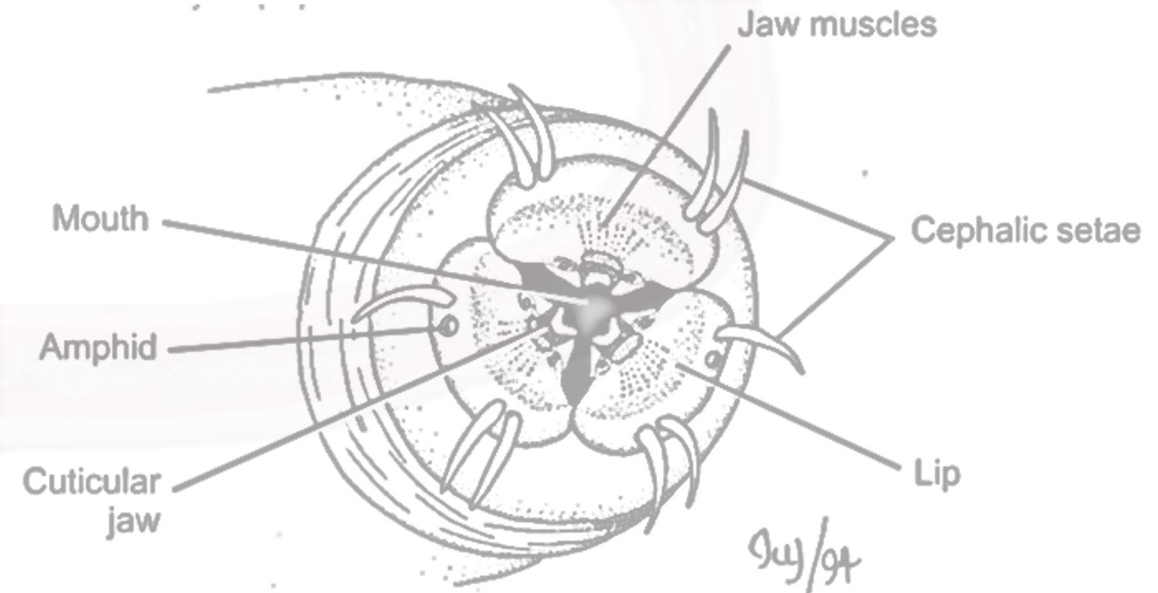
Adult *Brugia malayi* are long and slender with a smooth cuticle, kinked, and has a long cephalic space having a length:

width ratio of about 2:1.

The head is slightly swollen.

The tail of *B. malayi* is ventrally curved.

Sexual dimorphism exists with the adult female *B. malayi* being approximately 8 cm long by 0.3 mm wide and the male about 2 cm long and 0.1 mm wide.



Parasitism

- It cause elephantiasis and river blindness, cause chronic, debilitating infection

- **Geographic distribution**

In Southeast Asia and Indonesia



Life cycle

During a blood meal, an infected mosquito introduces third-stage filarial larvae onto the skin of the human host, where they penetrate into the bite wound.

The microfilariae migrate into lymph and enter the blood stream reaching the peripheral blood.

After ingestion, the microfilariae lose their sheaths and work their way through the wall of the proventriculus and cardiac portion of the midgut to reach the thoracic muscles.

A mosquito ingests the microfilariae during a blood meal.

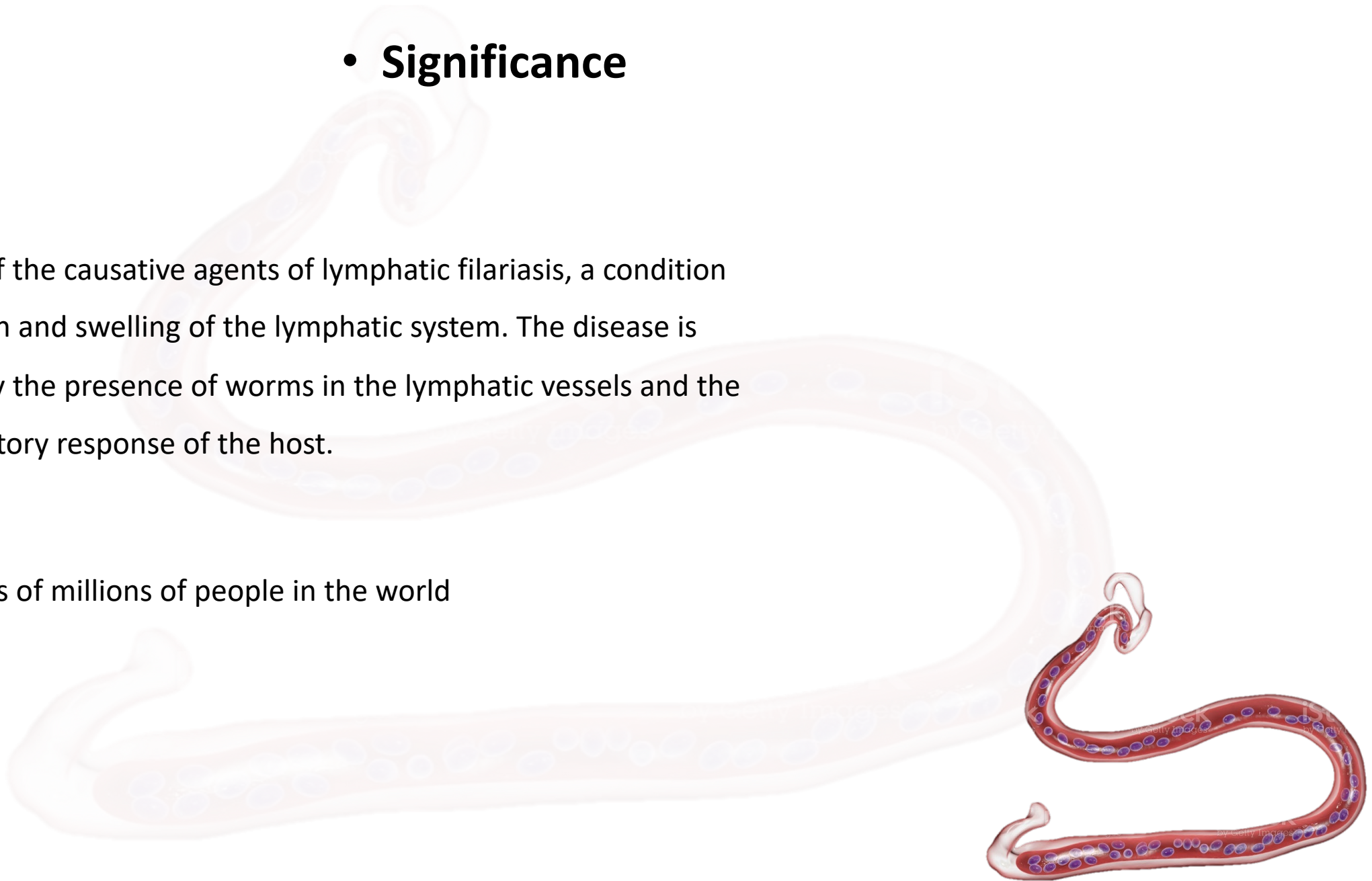
There the microfilariae develop into first-stage larvae and subsequently into third-stage larvae.

The third-stage larvae migrate through the hemocoel to the mosquito's proboscis and can infect another human when the mosquito takes a blood meal.

• Significance

▮ *B. malayi* is one of the causative agents of lymphatic filariasis, a condition marked by infection and swelling of the lymphatic system. The disease is primarily caused by the presence of worms in the lymphatic vessels and the resulting inflammatory response of the host.

- Threaten hundreds of millions of people in the world



- **Sequenced samples information**

The source was not included in the paper

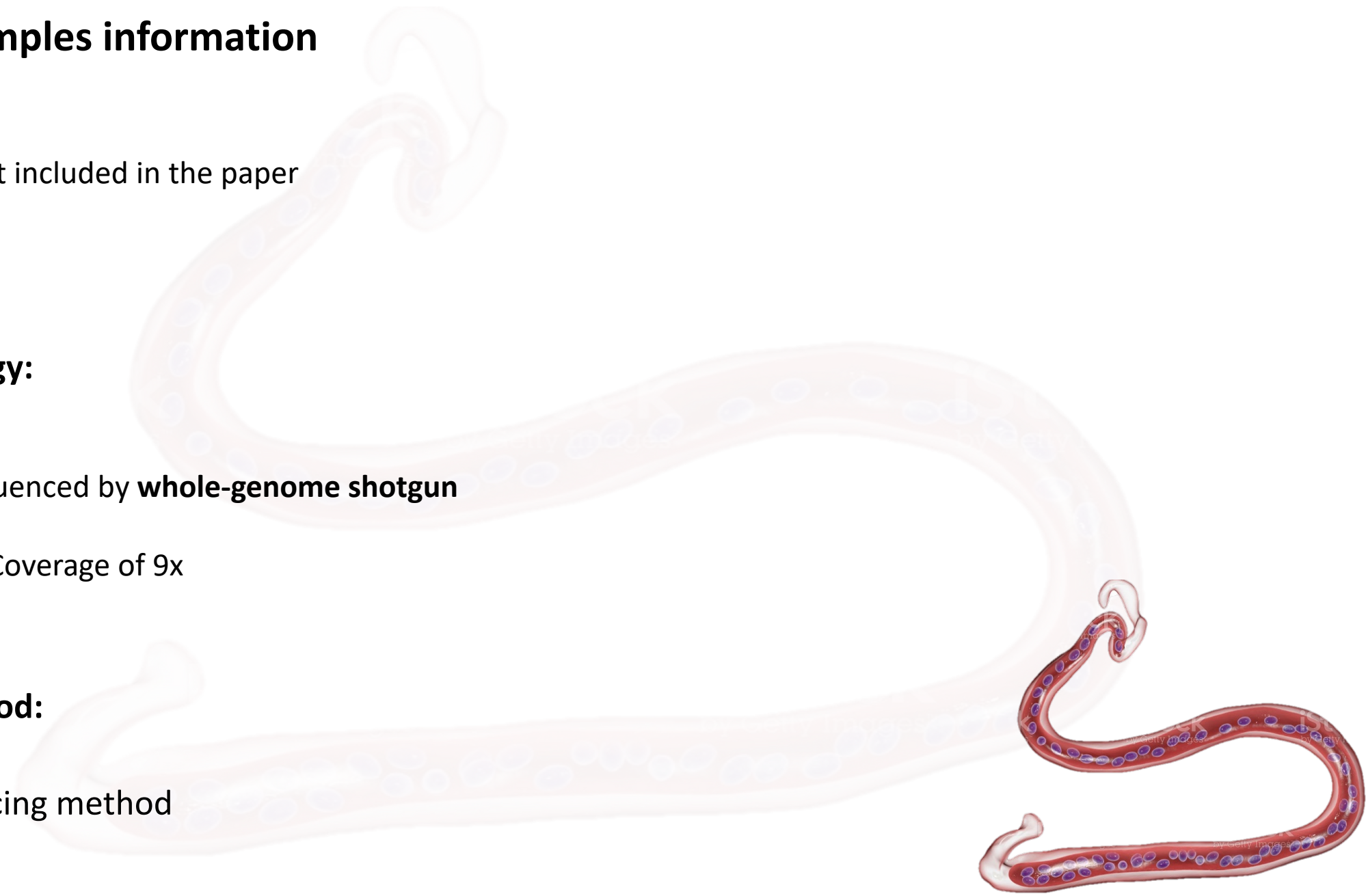
- **Sequencing strategy:**

The genome was sequenced by **whole-genome shotgun**

Coverage of 9x

- **Sequencing method:**

Sanger sequencing method

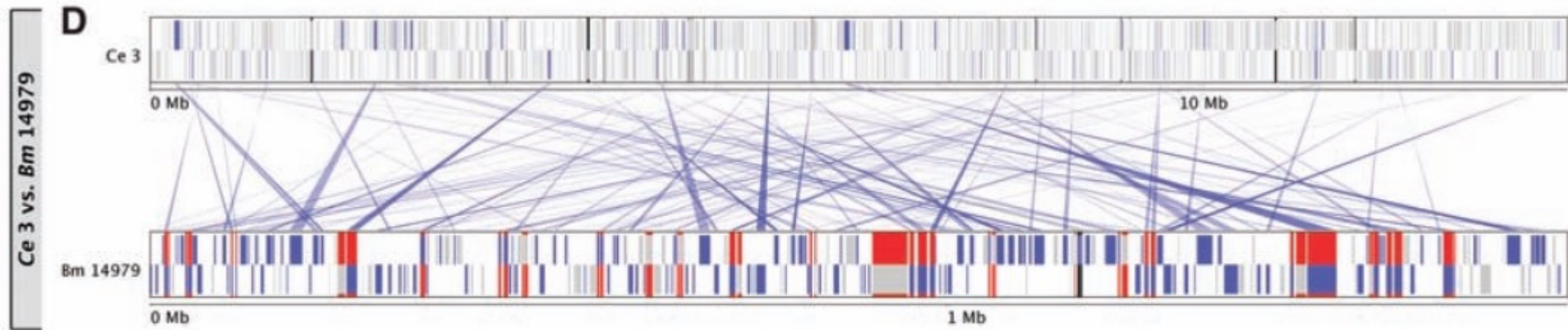




- **Genome assembly**

Features	<i>B. malayi</i>	<i>C. elegans</i>
Overall		
Estimated size of genome (Mb)	90–95	
Total number of bp of assembled sequence (bp)	88,363,057	
Number of scaffolds	8,180	
N50 of scaffolds (bp)	93,771	
Maximum length of scaffold (bp)	6,534,162	
Number of bp assembled into scaffolds (bp)	70,837,048	
Number of orphan contigs	18,868	

- Interesting genome outcome



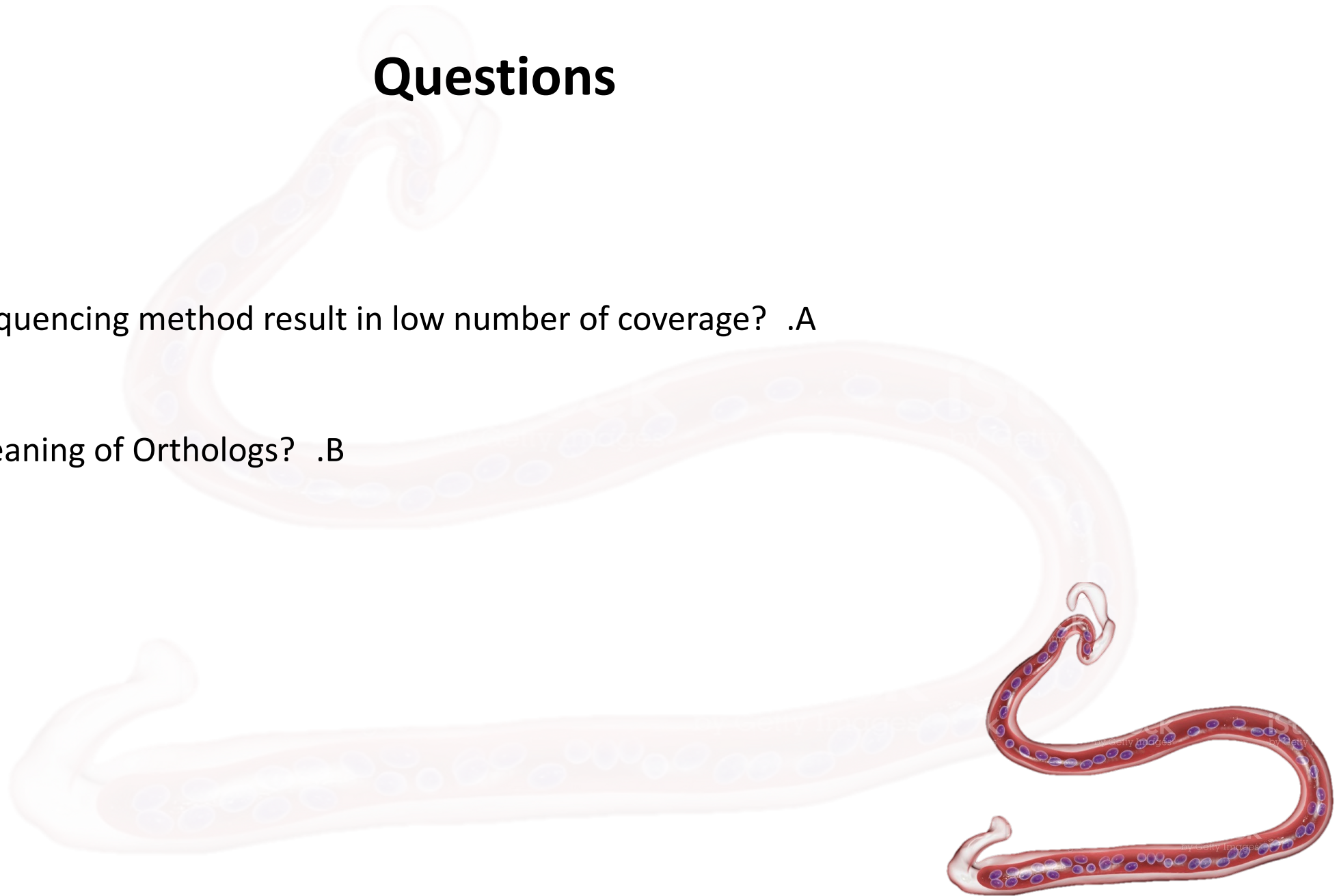
Relative arrangements of the genes on *B. malayi* scaffold 14979 and their orthologs on *C. elegans* chromosome 3. Forward and reverse-strand genes are distinguished.

Red rectangles correspond to putative *B. malayi* operons.

Questions

Why sanger sequencing method result in low number of coverage? .A

What is the meaning of Orthologs? .B





The end

Thank you for listening

