



A look into genome of *Ancylostoma ceylanicum* a parasite to human

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Intro to genomics – 485
20/1/2022



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The genome and transcriptome of the zoonotic hookworm *Ancylostoma ceylanicum* identify infection-specific gene families

Erich M Schwarz¹, Yan Hu^{2,3}, Igor Antoshechkin⁴, Melanie M Miller³, Paul W Sternberg^{4,5} & Raffi V Aroian^{2,3}

Hookworms infect over 400 million people, stunting and impoverishing them^{1–3}. Sequencing hookworm genomes and finding which genes they express during infection should help in devising new drugs or vaccines against hookworms^{4,5}. Unlike other hookworms, *Ancylostoma ceylanicum* infects both humans and other mammals, providing a laboratory model for hookworm disease^{6,7}. We determined an *A. ceylanicum* genome sequence of 313 Mb, with transcriptomic data throughout infection showing expression of 30,738 genes. Approximately 900 genes were upregulated during early infection *in vivo*, including ASPRs, a cryptic subfamily of activation-associated secreted proteins (ASPs)⁸. Genes downregulated during early infection included ion channels and G protein-coupled receptors; this downregulation was observed in both parasitic and free-living nematodes. Later, at the onset of heavy blood feeding, C-lectin genes were upregulated along with genes for secreted clade V proteins (SCVPs), encoding a previously undescribed protein family. These findings provide new drug and vaccine targets and should help elucidate hookworm pathogenesis.

closely related to the free-living *Caenorhabditis elegans* than is the free-living *Pristionchus pacificus* (Fig. 2)^{12–15}. Treatments effective against *A. ceylanicum* might thus also prove useful against other strongylids, such as *Haemonchus contortus*, that infect farm animals and depress agricultural productivity¹⁶. Characterizing the genome and transcriptome of *A. ceylanicum* is a key step toward such comparative analysis.

We assembled an initial *A. ceylanicum* genome sequence of 313 Mb and a scaffold N50 of 668 kb, estimated to cover ~95% of the genome, with Illumina sequencing and RNA scaffolding^{17,18} (Supplementary Tables 1–3). The genome size was comparable to those of *Ancylostoma caninum* (347 Mb)¹⁹ and *H. contortus* (320–370 Mb)^{20,21} but larger than those of *N. americanus*, *C. elegans* and *P. pacificus* (100–244 Mb)^{22–24}. We found that 40.5% of the genomic DNA was repetitive, twice as much as in *N. americanus*, *C. elegans* or *P. pacificus* (17–24%). We predicted 26,966 protein-coding genes²⁵ with products of ≥100 residues (Supplementary Table 4). We also predicted 10,050 genes with products of 30–99 residues, to uncover smaller proteins that might aid in parasitism²⁶. With RNA sequencing (RNA-seq), we detected expression of 23,855 (88.5%) and 6,883 (68.5%) of these genes, respectively (Fig. 3).

A. ceylanicum Taxonomy

- K: Animalia
 - P: Nematoda
 - C: Chromadorea
 - O: Rhabditida
 - F: Ancylostomatidae
 - G: *Ancylostoma*
 - S: *A. ceylanicum*

A. ceylanicum: History & Discovery

- Discovered in 1911 by Arthur Looss.
- Studying bilharzia in Egypt.
- *A. braziliense* and *A. ceylanicum* was considered synonymous due to the apparent similarities in almost all respects.
- In 1951, Biocca made study and he could identify between the two species.



A. ceylanicum: Physical characteristic

- parasitic roundworm .
- about 6–10 mm long.
- Life span from 1-15 years
- Have a mouth like other hookworm with cutting plate with a sharp dorsal end
- **Female** :tapered narrow posterior end
- **Male**: have a feathery posterior end.



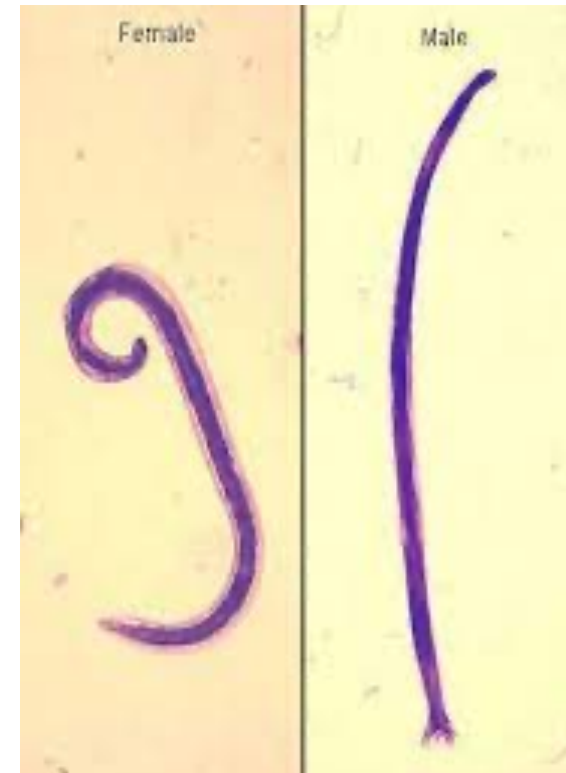
Ancylostoma duodenale



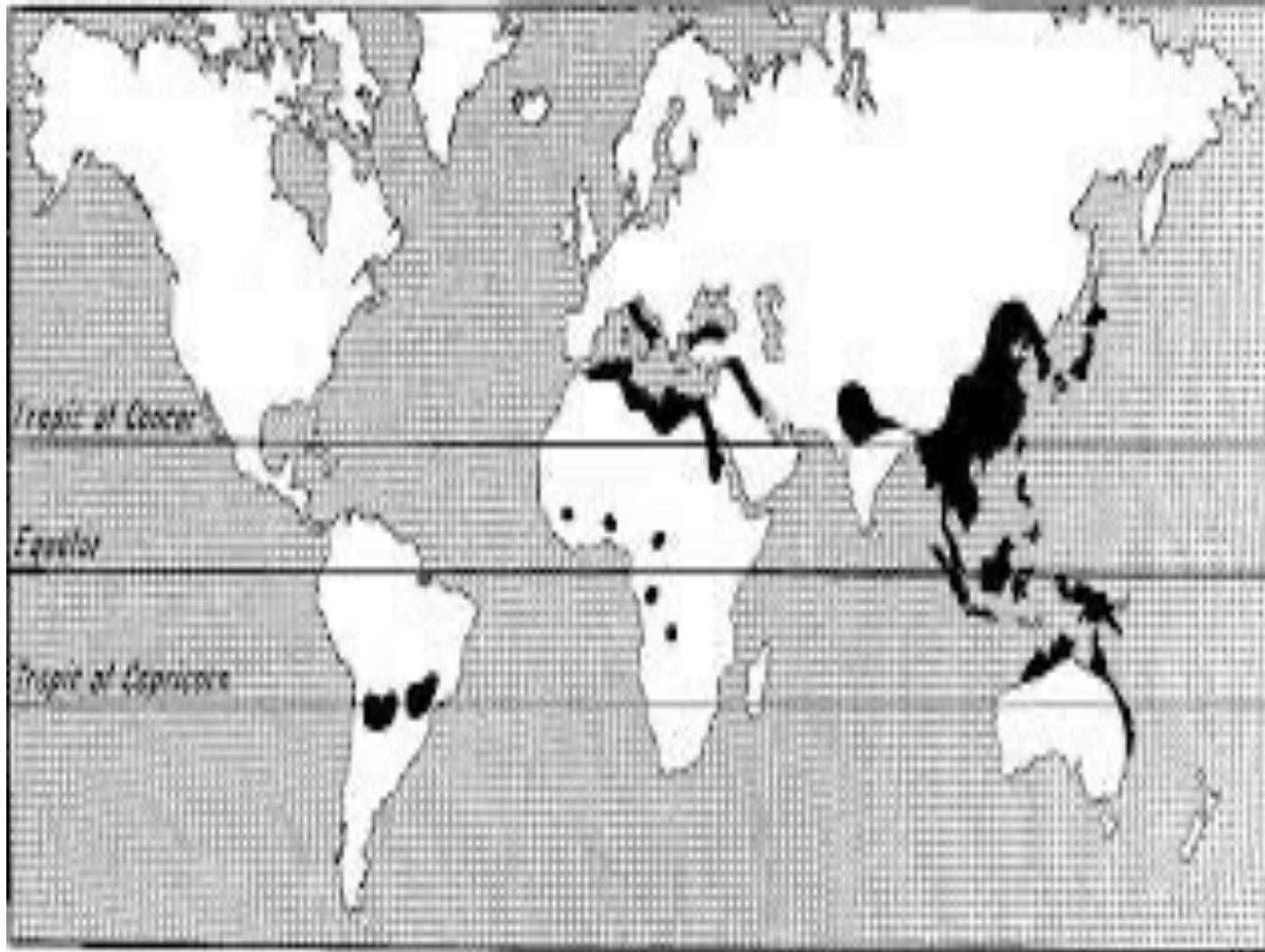
Ancylostoma ceylanicum



Necator americanus



A. ceylanicum: Geographic distribution



***A. ceylanicum*: infection information**

- *A. ceylanicum* enter to the host by burrowing into skin.
- Pass with the bloodstream until it leads to the small intestine.
- In small intestine it feed on the blood and **causing anemia**.
- accompanied significant loss in body weight.
- It may cause iron deficiency, hypoalbuminemia, in addition to anemia.

***A. ceylanicum*: Parasitism**

- ***A. ceylanicum* does not have an intermediate host. Therefore human can be primary host.**
- **Can be seen in the skin of the host.**



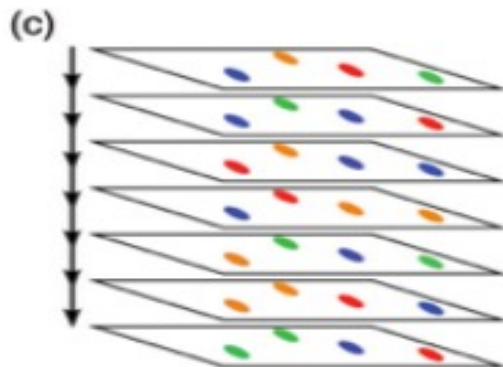
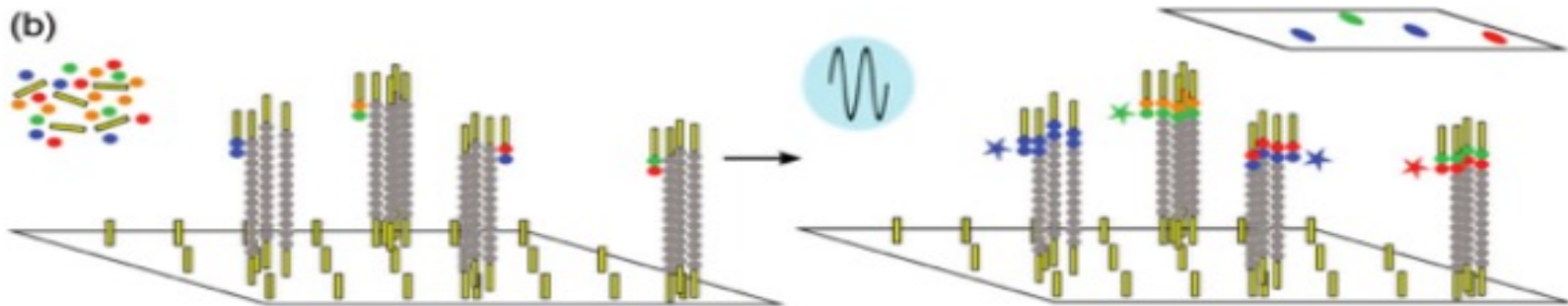
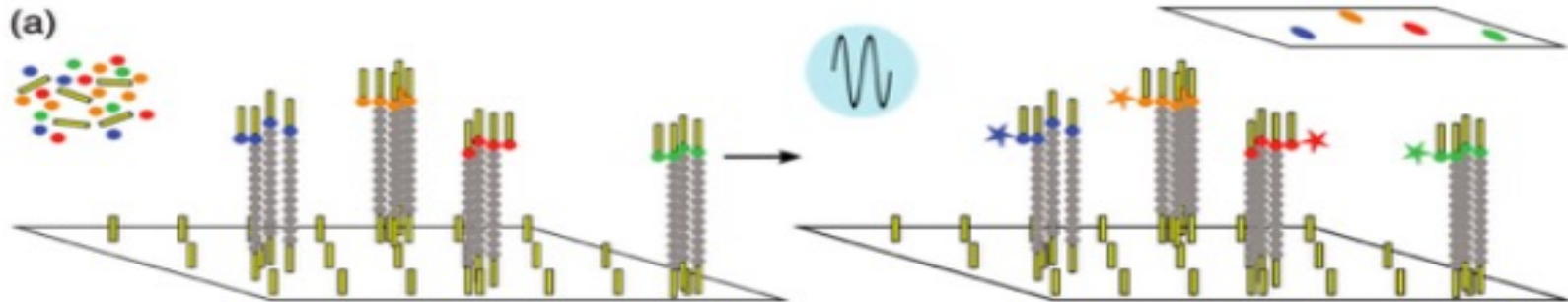
A. ceylanicum: Sequencing sample info

- All specimens of *Ancylostoma ceylanicum* were collected from Golden Syrian hamsters.
- The Aroian laboratory strain of *A. ceylanicum* used in this work has been designated HY135



A. ceylanicum : Sequencing method

■ Illumina sequencing method



A. ceylanicum : Genome assembly

Supplementary Table 2: Characteristics of genome and cDNA assemblies.

	Genome assemblies					cDNA assembly (from RNA-seq)
	<i>A. ceylanicum</i>	<i>C. elegans</i>	<i>P. pacificus</i>	<i>N. americanus</i>	<i>H. contortus</i>	
Total nt:	313,110,363	100,286,401	172,494,865	244,075,060	369,846,877	64,318,273
Scaffolds:	1,737	7	18,083	11,864	23,860	332,724
Contigs:	32,171	7	33,305	65,213	65,523	332,724
ACGT nt:	300,908,004	100,286,401	153,192,245	208,173,610	346,042,478	64,318,273
N-res. nt:	12,202,359	0	19,302,620	35,901,450	23,804,399	0
% non-N:	96.1	100.0	88.8	85.3	93.6	100.0
% GC:	43.4	35.4	42.8	40.2	43.1	44.6
Scaffold N50 nt:	668,412.0	17,493,829.0	1,244,534.0	211,861.0	83,287.0	294.0
Scaffold N90 nt:	117,063.0	13,783,801.0	85,679.0	29,168.0	11,529.0	78.0
Scaf. max. nt:	4,802,298	20,924,180	5,268,024	1,890,151	947,606	10,003
Scaf. min. nt:	509	13,794	47	201	101	53
Contig N50:	18,451.0	17,493,829.0	18,131.0	5,429.0	20,808.0	294.0
Contig N90:	4,900.0	13,783,801.0	2,062.0	1,285.0	4,267.0	78.0
Contig max. nt:	125,366	20,924,180	163,374	62,795	135,785	10,003
Contig min. nt:	1	13,794	1	25	1	53

Statistics are shown for the *A. ceylanicum* genome and cDNA assemblies, along with genome assemblies from the closely related nematodes *C. elegans*, *P. pacificus*, *N. americanus*, and *H. contortus*. Assemblies from related nematodes were from WormBase release WS242. For *H. contortus*, we used the genome assembly of Laing et al.^{S22}.

-Genomic assembly

- Contigs= 32 Kb
- Genome size = 347 Mb
- Scaffolds = 1 kb
- Scaffolds N50 = 668 Kb

-cDNA assembly

- Contigs= 332 kb
- Genomic size=64 Mb
- Scaffolds= 332 kb
- Scaffolds N50=294

***A. ceylanicum* : Interesting genome outcome**

- About 40.5% of the genomic DNA was repetitive.
- The GC% was about 43.4% for genomic DNA while 44.6 for cDNA.

Questions

1. **What is the intermediate host of *A. ceylanicum*?**
2. **what was the sequencing method that was used and give a brief description about the steps?**

**Thank You for
Listening**

