

A look into genome of *L. loa* a parasite to human

Mehdi Ghaedi Intro to genomics – 485 18/01/2022



Outline

- Selected paper
- Loa loa
 - Taxonomy
 - Physical characteristic
 - Inflectional information.
 - Parasitism
 - Geographic distribution
 - Life cycle
 - Significance
- Sequencing sample information
- Sequencing strategy
- Sequencing method
- Genome assembly
- Interesting genome outcome

Selected paper

ARTICLES

nature genetics OPEN

Genomics of *Loa loa*, a *Wolbachia*-free filarial parasite of humans

Christopher A Desjardins¹, Gustavo C Cerqueira¹, Jonathan M Goldberg¹, Julie C Dunning Hotopp², Brian J Haas¹, Jeremy Zucker¹, José M C Ribeiro³, Sakina Saif¹, Joshua Z Levin¹, Lin Fan¹, Qiandong Zeng¹, Carsten Russ¹, Jennifer R Wortman¹, Doran L Fink^{4,5}, Bruce W Birren¹ & Thomas B Nutman⁴

Loa loa, the African eyeworm, is a major filarial pathogen of humans. Unlike most filariae, L. loa does not contain the obligate intracellular Wolbachia endosymbiont. We describe the 91.4-Mb genome of L. loa and that of the related filarial parasite Wuchereria bancrofti and predict 14,907 L. loa genes on the basis of microfilarial RNA sequencing. By comparing these genomes to that of another filarial parasite, Brugia malayi, and to those of several other nematodes, we demonstrate synteny among filariae but not with nonparasitic nematodes. The L. loa genome encodes many immunologically relevant genes, as well as protein kinases targeted by drugs currently approved for use in humans. Despite lacking Wolbachia, L. loa shows no new metabolic synthesis or transport capabilities compared to other filariae. These results suggest that the role of Wolbachia in filarial biology is more subtle than previously thought and reveal marked differences between parasitic and nonparasitic nematodes.

Loa loa: Taxonomy

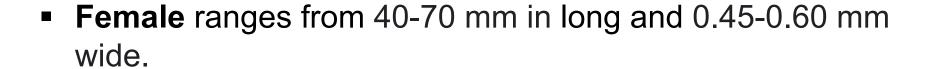
- SK: Eukaryota
 - K: Metazoa
 - P: Nematoda
 - C: Chromadorea
 - O: Rhabditida
 - SO: Spirurina
 - F: Onchocercidae
 - G: Loa
 - S: loa

Loa loa: Physical characteristic

Round worm nematodes.

Cylindrical shape + irregular curves.





- Male ranges at 30-34 mm long and 0.35-0.40 mm wide.
- Microfilariae (wormlike eggs) 250–300 μm (0.25mm) long, 6–8 μm wide.

Loa loa: Physical characteristic



Loa loa: Inflectional information

chronic infection and affects around 13 million people.

Cause <u>Loiasis</u>

angioedema or subconjunctival migration.

Encephalopathy and entrapment neuropathy

Loa loa: Parasitism

Intermediate host = Chrysops (deerfly)



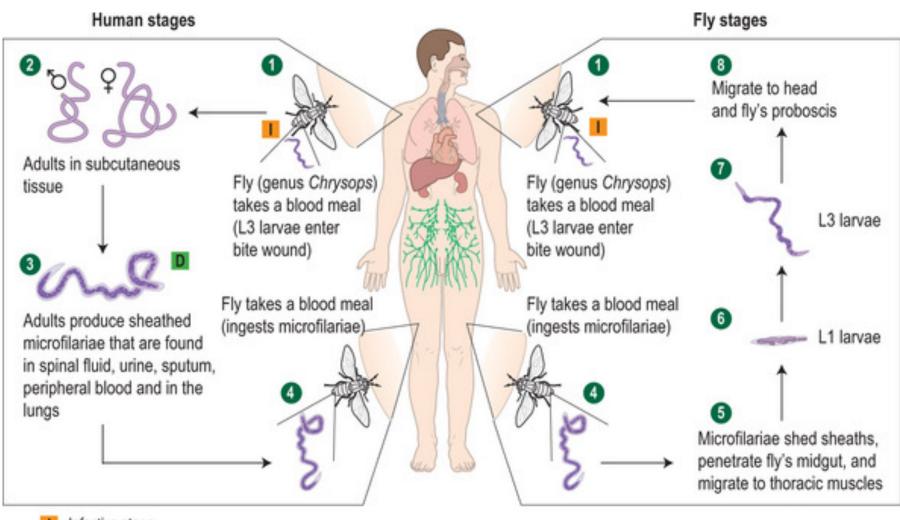
Definitive host human and can be seen in eye (only as adult form).

Loa loa: Geographic Distribution

L. loa is restricted
geographically to equatorial
west and central Africa,
where its deerfly vector
Chrysops spp breeds.



Loa loa: Life cycle



- I Infective stage
- Diagnostic stage

^{*}L3 infective larvae

Loa Ioa: Significance

 Adverse events (encephalopathy and death) after using ivermectin treatment.

Lack of endosymbionts Wolbachia.

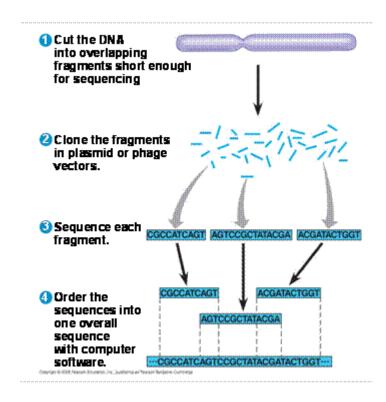
 Gaining clinical information about post-treatment reaction.

Loa loa: Sequencing sample information

- Microfilariae of L. loa were purified from a patient infected in Cameroon.
- Single unfertilized adult W. bancrofti worm was under ultrasonic guidance.
- O. volvulus single adult male was isolated from nodule in Ecuador.

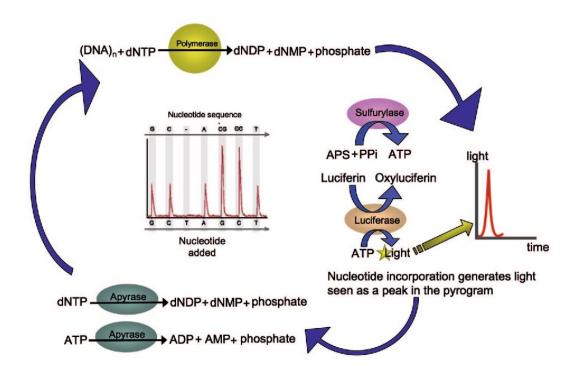
Loa loa: Sequencing strategy

Whole genome shotgun Sequencing



Loa loa: Sequencing method

- Pyrosequencing
- Roche 454 life sciences



Loa loa: Genome assembly

Table 1 Genome features of filarial worms and their Wolbachia endosymbionts

Organism	Coverage	Sequence (Mb)	Scaffolds	Scaffold N50 (kb)	GC (%)	Repetitive (%)	Low complexity (%)	Genes (n)
L. loa	20×	91.4	5,774	172	31.0	9.3	1.7	14,907a
W. bancrofti	12×	81.5	25,884	5.16	29.7	6.2	3.9	19,327a
O. volvulus	5×	26.0	22,675	1.27	32.5	-	-	-
B. malayi	9x	93.7	8,180	94	30.2	12.1	1.1	18,348

- Coverage = 20x
- Genome size = 91.4 Mb
- Scaffolds = **5774**
- Scaffolds N50 = 172 Kb

Loa loa: Interesting genome outcome

• O. volvulus genome was not included in further analyses.

L. loa was assembly was the most contagious between them.

No large transfers of <u>nuwts</u> was revealed in *L. loa* genome.

Questions

1. Does *L. loa* necessarily cause blindness?

2. why do you think pyrosequencing was used as sequencing method?













Thank You for Listening

