



wellcome
connecting
science



Helminth Bioinformatics Latin America & the Caribbean

Montevideo, Uruguay
18–24 May 2025

Jose Tort



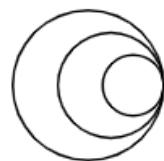
UNIVERSIDAD
DE LA REPÚBLICA
URUGUAY



INSTITUTO DE HIGIENE
Prof. Arnoldo Berta
FACULTAD DE MEDICINA

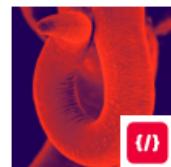


FACULTAD DE
MEDICINA



Global Training

Building capacity in biomedicine for research and healthcare communities in Latin America, Africa and Asia.



Helminth Bioinformatics - Latin America & the Caribbean

18–24 May 2025

Deadlines: all closed



Polygenic Risk Score Analysis - Africa

22–27 June 2025

Deadlines: all closed



Genomics and Epidemiological Surveillance of Bacterial Pathogens - Latin America and the Caribbean

6–11 July 2025

Deadlines: all closed



Single Cell Technologies: Practical Approaches Advancing Research - Latin America and the Caribbean

10–16 July 2025

Deadlines: all closed

[Our events](#)

[Conferences](#)

[Courses](#)

[COG-Train Programme](#)

[Global Training](#)

[Online courses](#)

[Past events](#)

[Your digital mentor podcast](#)

[Accessibility information](#)

[FAQ](#)

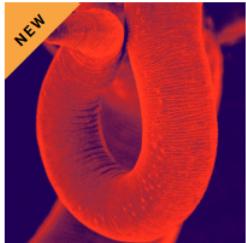
WCS global training

- 2006** First Joint Wellcome-Pasteur course on Genomics
Inauguration of the IH Bioinfo facilities
- More than 20 courses held so far
- 2007** First Pathogen Genomes LATAM
(repeated 7 times!!!)



Helminth Bioinformatics

[Home](#) / [Our events](#) / [Past events](#) / [Global training](#) / Helminth Bioinformatics (Accra, Ghana)

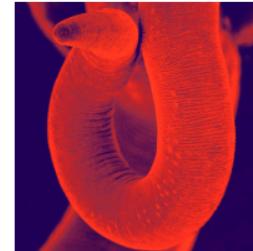


Helminth Bioinformatics (Accra, Ghana)

8–13 September 2019

West African Centre for Cell Biology of Infectious Pathogens (WACCBIP), University of A
Ghana

[Home](#) / [Our events](#) / [Global training](#) / Helminth Bioinformatics (Asia) (Virtual)



(helminthomics)

Helminth Bioinformatics (Asia) (Virtual)

28 June–2 July 2021

Virtual Course

[Home](#) / [Our events](#) / [Global training](#) / Helminth Bioinformatics - Asia



Helminth Bioinformatics - Asia

21–27 May 2023

Khon Kaen University, Thailand

[Home](#) / [Our events](#) / [Global training](#) / Helminth Bioinformatics - Latin America & the Caribbean



Helminth Bioinformatics - Latin America & the Caribbean

18–24 May 2025

Universidad de la Republica, Uruguay

Helminths

- (έλμινθος) worms (parasite)

ROUND



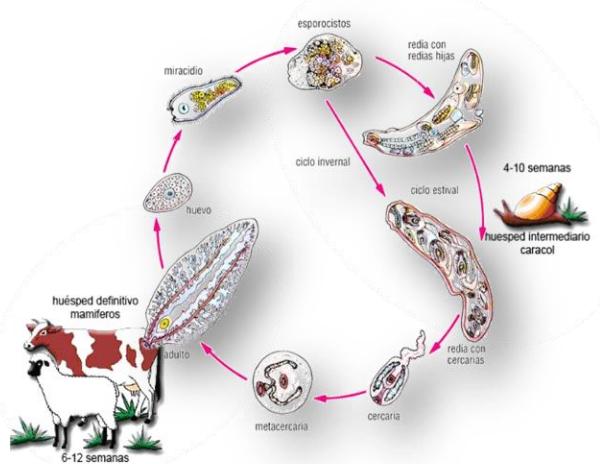
FLAT



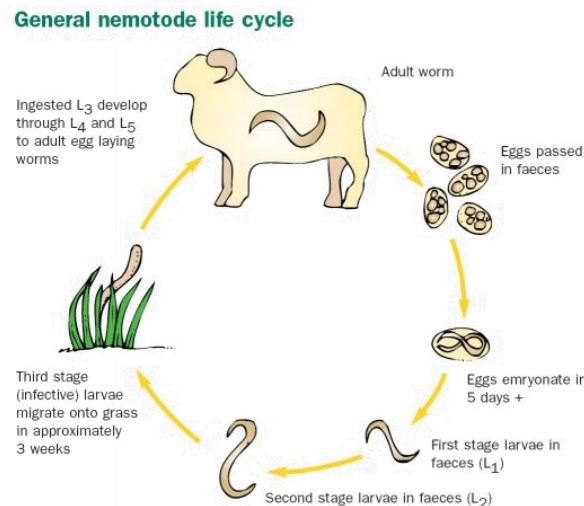
TAPE



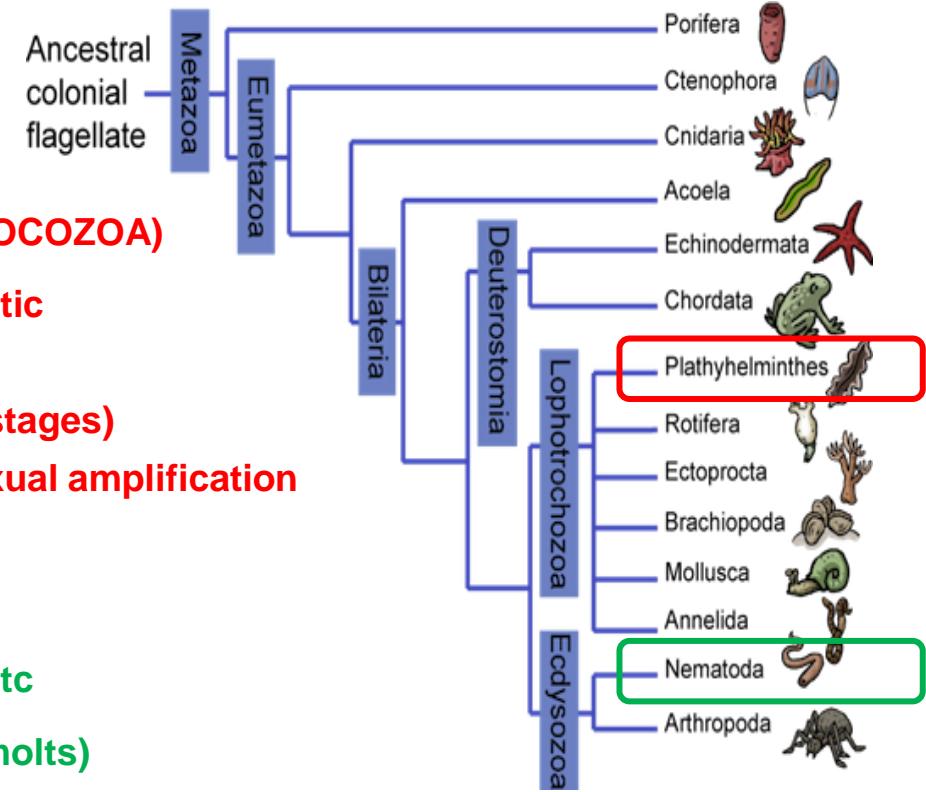
Helminths : Different metazoan lineages



- PLATYHELMINTHS (LOFOTROCOZOA)
- 15.000 / 20.000 species parasitic
- Biological plasticity
- Complex life cycles (diverse stages)
- Sexual reproduction and asexual amplification



- NEMATODES (ECDISOZOA)
- 20.000 / 80.000 species parasitic
- Programmed development (molts)
- Simple life cycles (similar stages)

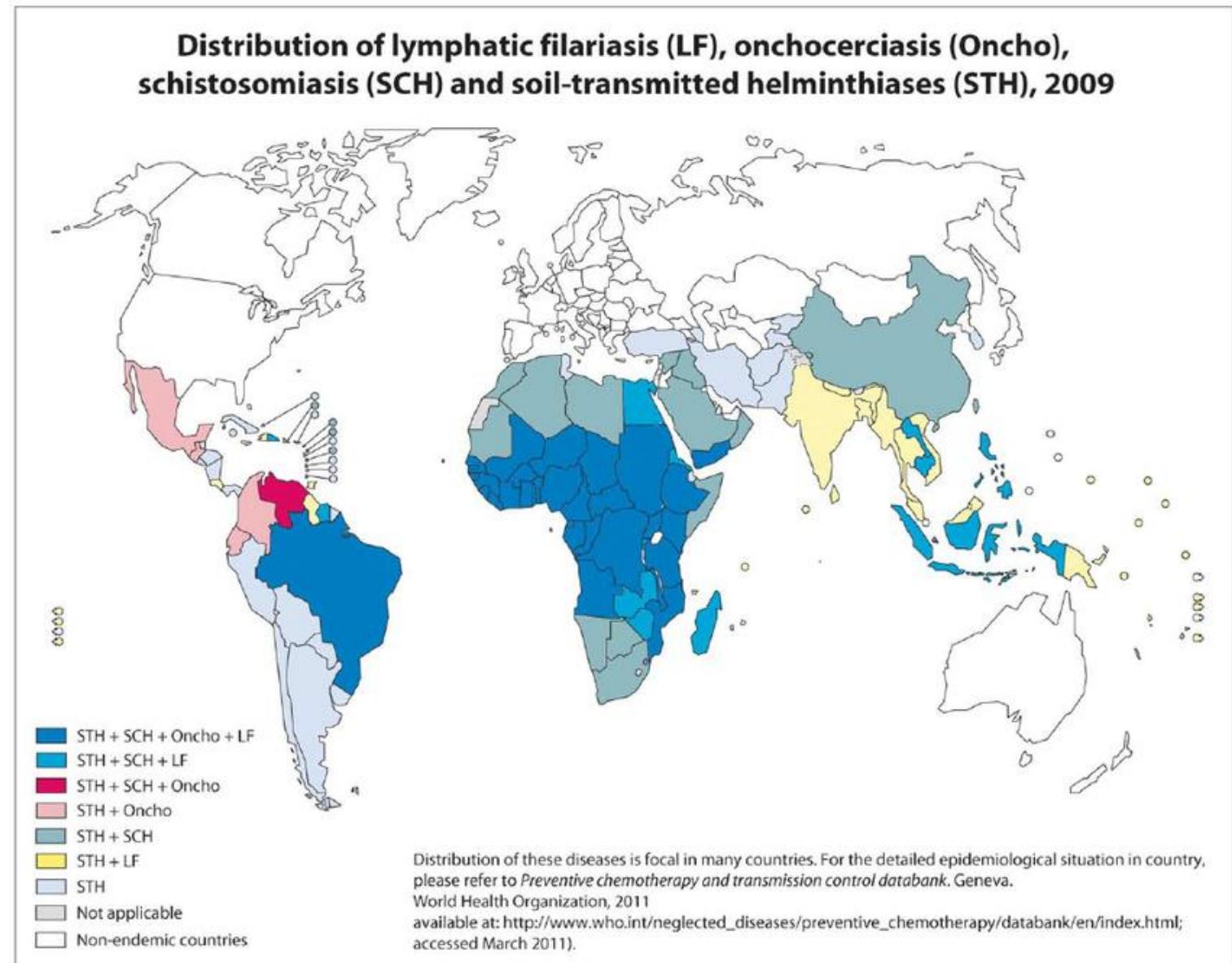


Parasitism as a way of life



Responsible for neglected diseases

- Chronic diseases
- High morbidity, low mortality
- High prevalence
- “Developing” regions of the world



Responsible of “neglected diseases”

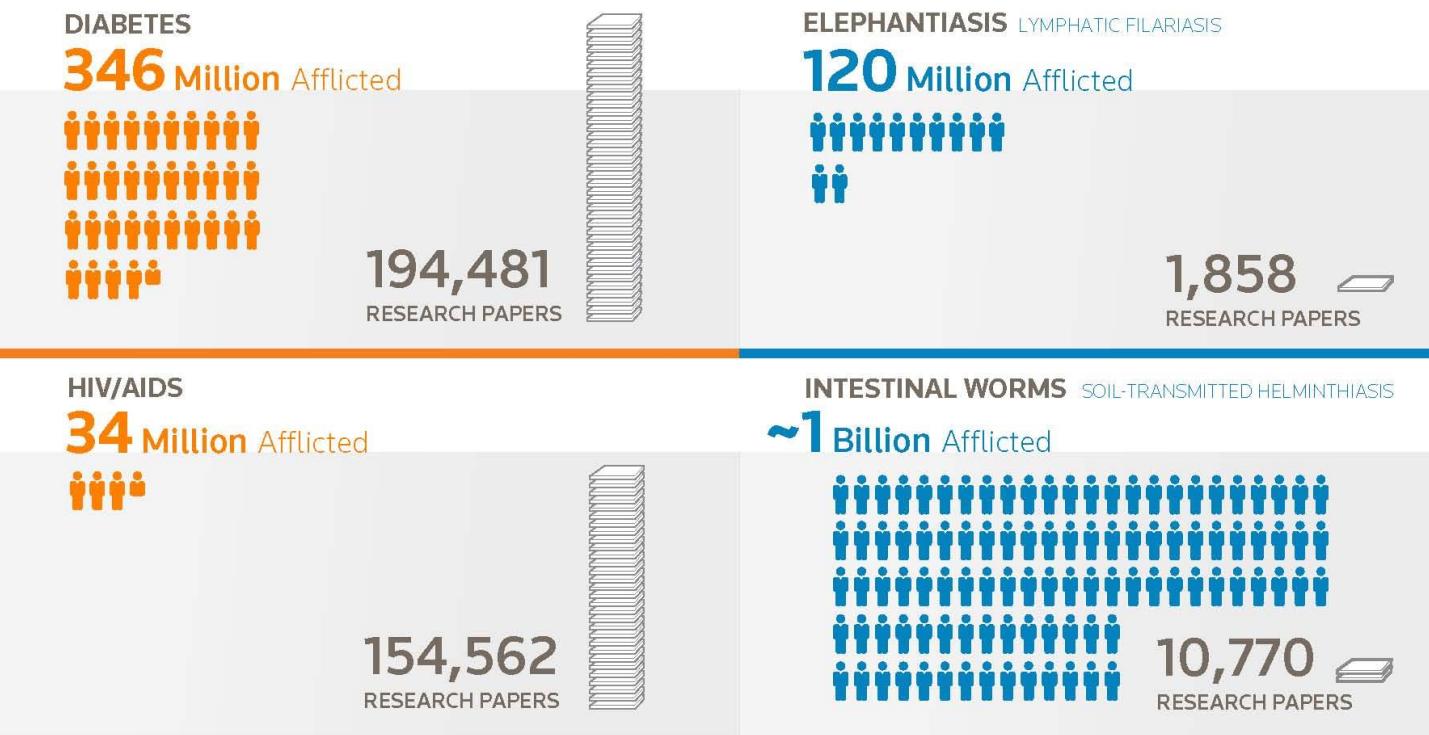
WHAT DOES IT MEAN TO BE “NEGLECTED”?



Neglected Tropical Diseases impact daily life for billions of people globally. However, funding for research and treatment of them pales in comparison to “first-world impacted or supported” diseases such as HIV/AIDS.

Social and moral questions arise when trying to understand why some diseases are favored over others, adding a new perspective on what it means to be truly neglected.

Thomson Reuters Global Research Report: *Neglected Tropical Diseases*
<http://researchanalytics.thomsonreuters.com/grr/>



Sources: Thomson Reuters Web of Knowledge, World Health Organization



Control measures

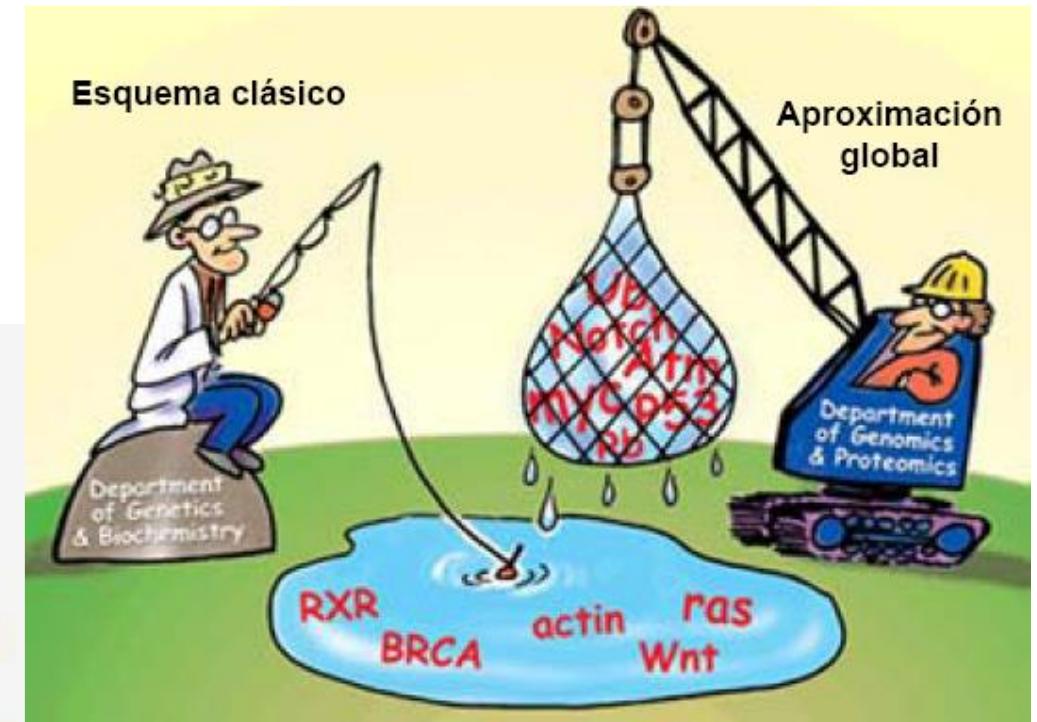
- **Chemotherapy**
 - Effective drugs but expensive
 - High rates of reinfection
 - Treatment does not impede damages
 - Drug resistance emerging

- **Vaccines**

- Variable effectiveness
- High costs
- Target selection



- **Search for new targets**



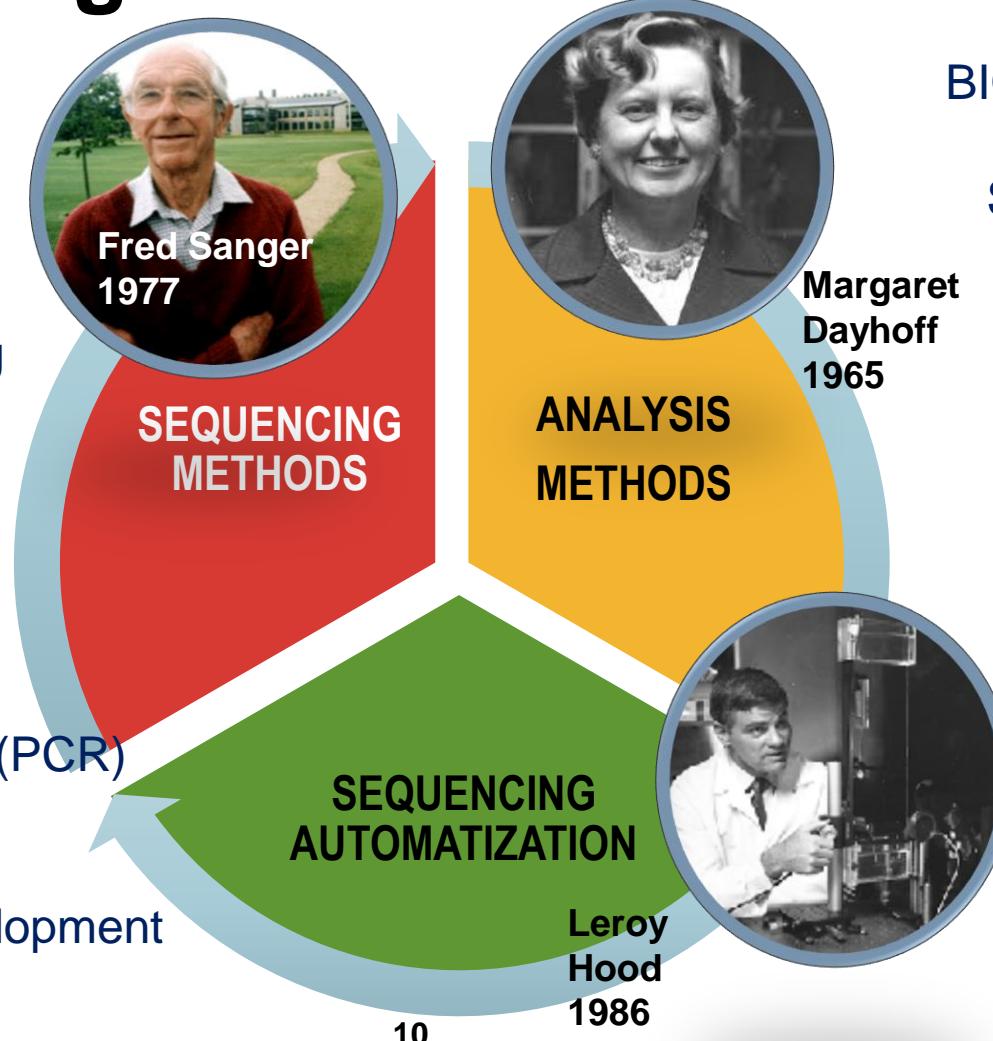
The pathway to genome sequencing

MOLECULAR TOOLS

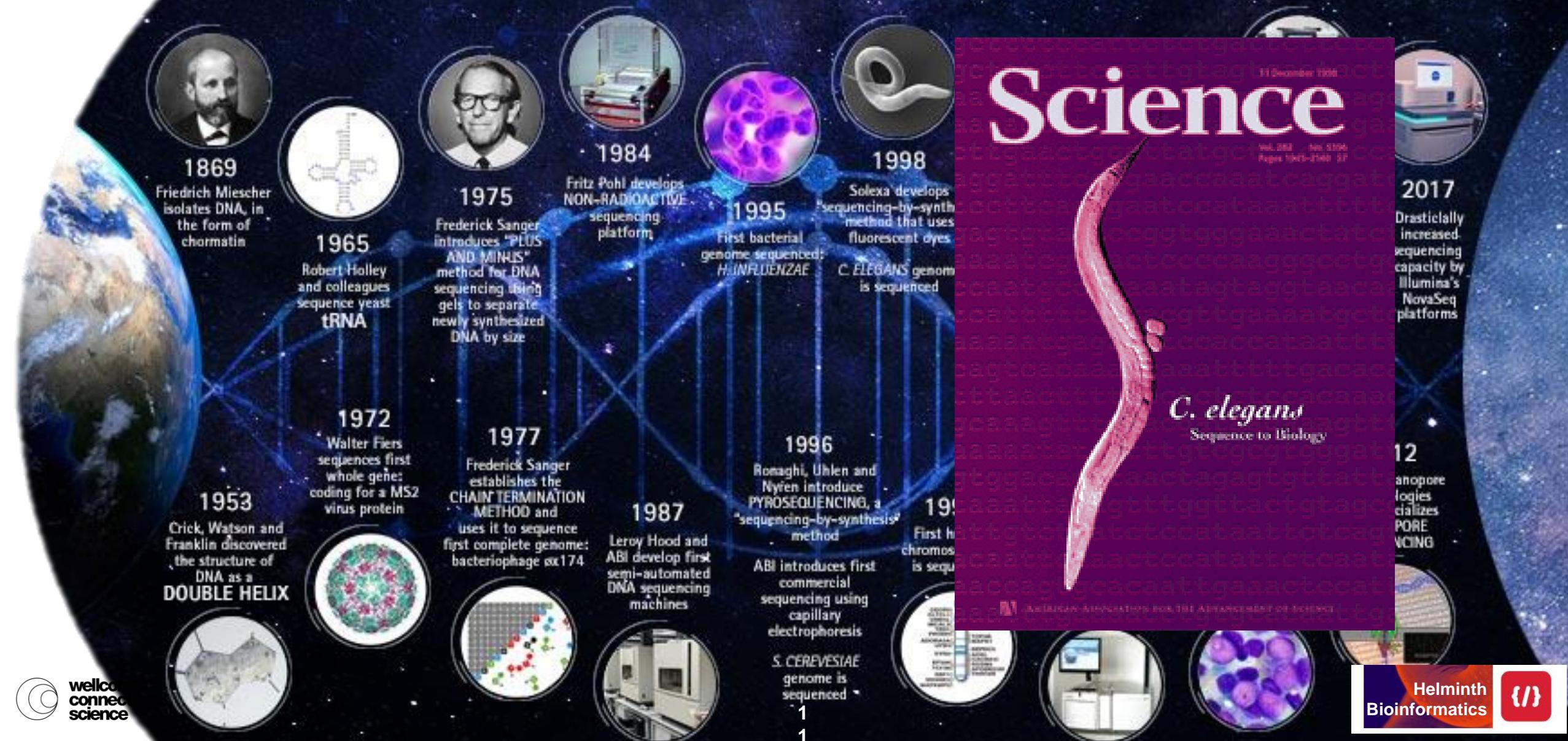
Purified Polymerases
In vitro reactions
DNA Radioactive labeling
Gel Electrophoresis
DNA cloning

TECHNOLOGY ADVANCES

Polymerase Chain Reaction (PCR)
Fluorescent labelling
Capillary electrophoresis
Sequencing equipment development

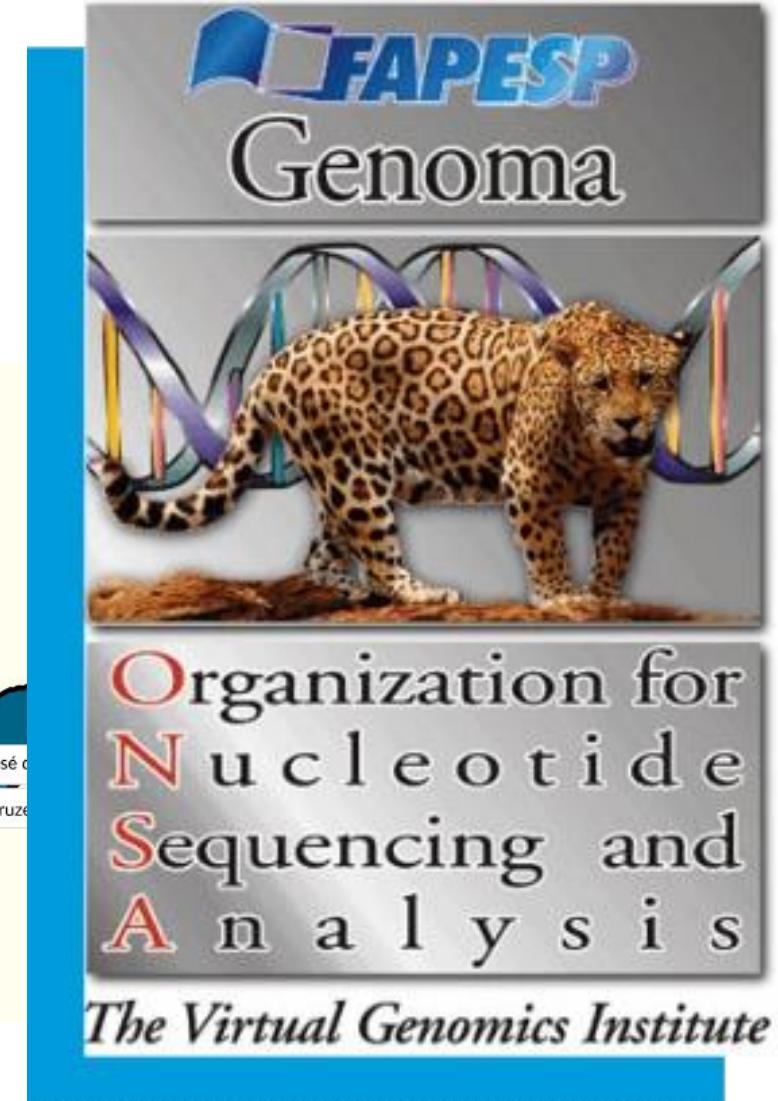
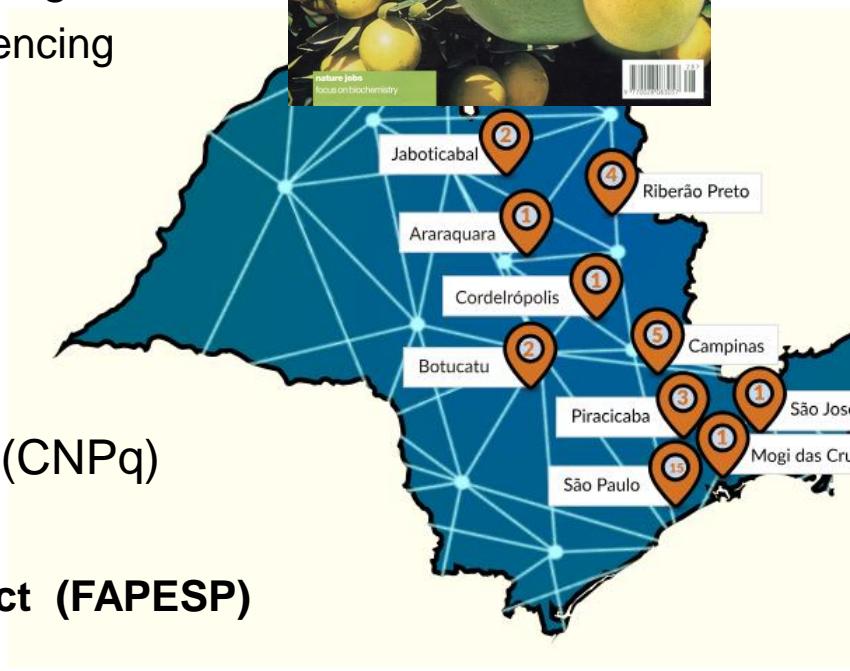


A JOURNEY THROUGH THE HISTORY OF DNA SEQUENCING



LATAM genomics : born in Brazil

- 1997 FAPESP releases **ONSA** program
Collaborative distributed sequencing
33 sequencing labs
2 bioinformatics center
- 2000 *Xylella fastidiosa* genome
([Simpson et al., 2000](#)).
- 2000 Rede Genomica Brasileira (CNPq)
- 2001 **Schistosoma Genome Project (FAPESP)**



<https://centrodememoria.fapesp.br/exposicoes/genoma/>

Trematode genomics started with transcriptomics projects

- Preferred to genomes (expressed genes vs gene structure)
- Gene expression at different stages
- Allow cloning relevant genes
- Provide information for other expression profiling approaches (i.e. arrays)
- Provide information for gene discovery algorithms.
- Needed for a proteomic approach to characterize molecules relevant in host-parasite relationship



ARTICLES

nature genetics

<http://bioinfo.iq.usp.br/schisto/>

Transcriptome analysis of the acelomate human parasite *Schistosoma mansoni*

Sergio Verjovski-Almeida¹, Ricardo DeMarco¹, Elizabeth A L Martins², Pedro E M Guimaraes³, Elida P B Ojopi³, Apula C M Paquola⁴, Joao P Piazza⁵, Milton Y Nishiyama Jr.⁴, Joao P Kitajima^{5,12}, Rachel E Adamson⁶, Peter D Ashton⁶, Maria F Bonaldo⁷, Patricia S Coulson⁸, Gary P Dillon⁹, Leonardo P Faria³, Sheila P Gregorio^{1,3}, Paulo L Ho³, Ricardo A Leite⁸, L Cosme C Malagueta⁹, Regina C P Marques⁸, Patricia A Miyasato¹⁰, Ana L T O Nascimento², Fernanda P Ohlweiler¹⁰, Eduardo M Reis^{1,11}, Marcela A Ribeiro¹¹, Renata G Sa¹², Gaelle C Stukart³, M Bento Soares^{7,13}, Cybele Gargioni¹⁴, Toshie Kawano¹⁰, Vanderlei Rodrigues¹², Alida M B N Madeira¹¹, R Alan Wilson⁶, Carlos F M Menck⁸, Joao C Setubal⁵, Luciana C C Leite² & Emmanuel Dias-Neto³

Schistosoma mansoni is the primary causative agent of schistosomiasis, which affects 200 million individuals in 74 countries. We generated 163,000 expressed-sequence tags (ESTs) from normalized cDNA libraries from six selected developmental stages of the parasite, resulting in 31,000 assembled sequences and 92% sampling of an estimated 14,000 gene complement. By analyzing automated Gene Ontology assignments, we provide a detailed view of important *S. mansoni* biological systems, including characterization of metazoan-specific and eukarya-conserved genes. Phylogenetic analysis suggests an early divergence from other metazoa. The data set provides insights into the molecular mechanisms of tissue organization, development, signaling, sexual dimorphism, host interactions and immune evasion and identifies novel proteins to be investigated as vaccine candidates and potential drug targets.

© 2003 Nature Publishing Group <http://www.nature.com/naturegenetics>

VOLUME 35 | NUMBER 2 | OCTOBER 2003 | NATURE GENETICS

148



Sanger Pathogen Unit

Pathogen Genome Sequencing

Bacteria:

All data from these projects are immediately and freely available.



Fungi:

All data from these projects are immediately and freely available.



Plasmids:

All data from these projects are immediately and freely available.



Bacteriophage:

All data from these projects are immediately and freely available.



Protozoa:

All data from these projects are immediately and freely available.



Parasitic Helminths:

All data from these projects are immediately and freely available.



Vectors:

All data from these projects are immediately and freely available.



Viruses:

All data from these projects are immediately and freely available.



Wellcome Sanger Institute
Berriman, Matt

Parasite Genomics



Welcome to the
GeneDB website
Version 2.1

The Wellcome Trust
Sanger Institute
Pathogen Sequencing Unit

Database Entry Point

Searches

Search for gene by ID/description in All organisms Include description in search Add wildcards to search term

Sequence Searches

omniBLAST (Multi-organism BLAST)

Datasets

Fungi

Protozoa

Parasitic Helminths

Bacteria Choose...
B. bronchiseptica
B. fragilis
B. parapertussis
B. pertussis
B. pseudomallei
C. abortus
C. diphtheriae
E. carotovora
S. aureus MRSA
S. aureus MSSA
S. coelicolor
S. typhi

Links

Prokaryotes
Eukaryotes (Fungi)
AC
Artemis

Go to our main search page, complex querying page, AmiGO or List Download

Information

Guide to GeneDB
What is GeneDB, and what's in it?
Navigating/Searchin GeneDB
Contacting Us/Feedback
Privacy Policy
Data Release Policy

PSU Sequencing Projects

Software

The GeneDB project is a core part of the Sanger Institute Pathogen Sequencing Unit's (PSU) activities. Its primary goals are:

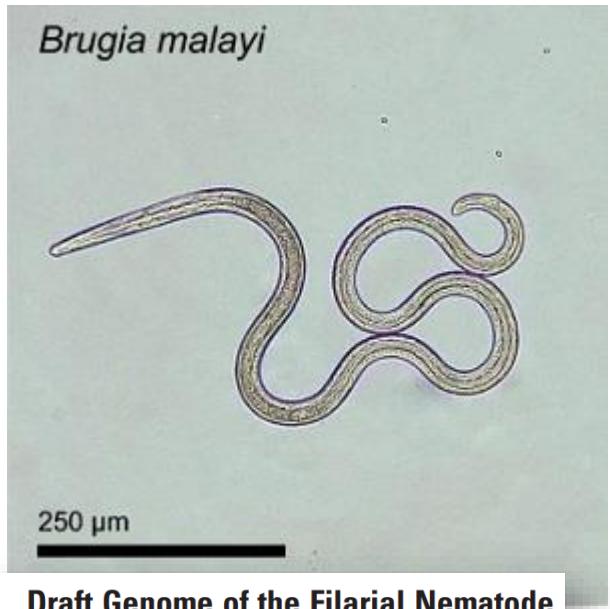
- to provide reliable access to the latest sequence data and annotation/curation for the whole range of organisms sequenced by the PSU.
- to develop the website and other tools to aid the community in accessing and obtaining the maximum value from this data.

GeneDB currently provides [access to 32 genomes](#), from various stages of the sequencing curation pipeline, from early access to partial genomes with automatic annotation through to complete genomes with extensive manual curation. We plan to add another 15 organisms over the next 6 months. (Details correct as of March 2005)



Parasitic helminths genomes

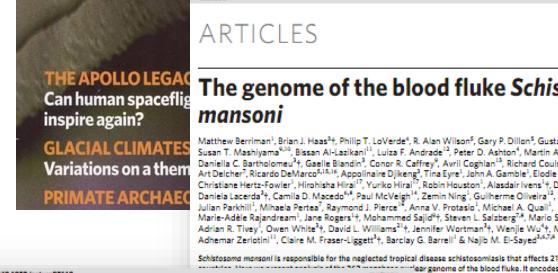
2007



Draft Genome of the Filarial Nematode Parasite *Brugia malayi*

Elodie Ghedin,^{1,2} Shiliang Wang,² David Spiro,² Elisabet Caler,² Qi Zhao,² Jonathan Crabtree,² Jonathan E. Allen,^{2*} Arthur L. Delcher,^{2†} David B. Guittard,³ Diego Miranda-Saaedra,^{4‡} Samuel V. Angiuoli,² Todd Creasy,² Paolo Amodeo,² Brian Haas,² Najib M. El-Sayed,^{2§} Jennifer R. Wortman,² Tamara Feldblyum,² Luke Tallon,² Michael Schatz,^{2†} Martin Shurway,² Hearn Koo,² Steven L. Salzberg,^{2†} Seth Schobel,² Michael Perteet,[†] Mihai Pop,[†] Owen White,² Geoffrey J. Barton,² Clotilde K. S. Carlow,⁵ Michael J. Crawford,⁶ Jennifer Daub,^{1||} Matthew W. Dimmic,³ Chris F. Estes,⁶ Jeremy M. Foster,⁵ Mehl Ganatra,⁵ William F. Gregory,⁷ Nicholas M. Johnson,⁹ Jimming Jin,¹⁰ Richard Komuniecki,¹¹ Ian Korf,¹² Sanjay Kumar,⁵ Sandra Laney,¹³ Ben-Wen Li,¹⁴ Wen Li,¹³ Tim H. Lindblom,⁸ Sara Lustigman,¹⁵ Dong Ma,⁵ Claude V. Maina,⁵ David M. A. Martin,⁴ James P. McCarter,^{6,16} Larry McReynolds,¹⁰ Makedonka Mitreva,¹⁶ Thomas B. Nutman,¹⁷ John Parkinson,¹⁸ José M. Peregrín-Alvarez,¹ Catherine Poole,⁵ Qinghu Ren,² Lori Saunders,¹³ Ann E. Studier,¹⁹ Katherine Smith,¹³ Mario Stanke,²⁰ Thomas R. Unnasch,²¹ Jenna Ware,⁵ Aguán D. Wei,²² Gary Weil,²⁴ Deryck J. Williams,⁷ Yinhua Zhang,⁵ Steven A. Williams,¹³ Claire Fraser-Liggett,¹¹ Barton Slakto,⁷ Mark L. Blaxter,¹ Alan L. Scott²³

2009

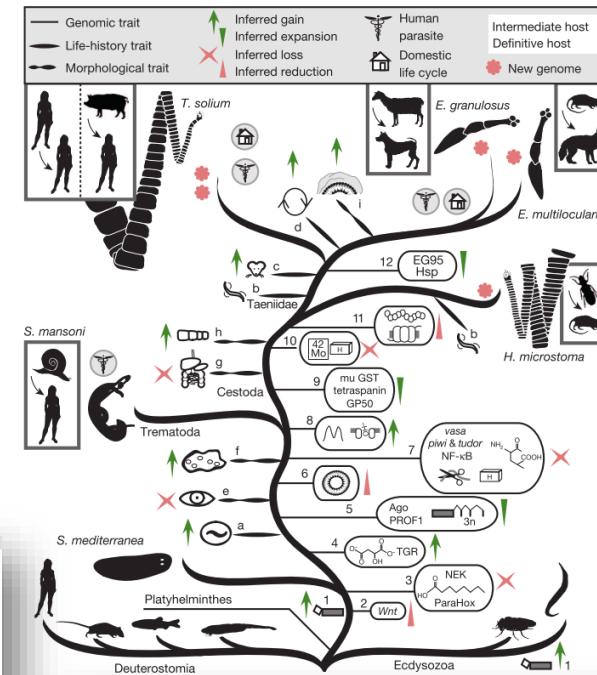


The *Schistosoma japonicum* genome reveals features of host-parasite interplay

The *Schistosoma japonicum* Genome Sequencing and Functional Analysis Consortium*

Schistosoma japonicum is a寄生虫 that causes human schistosomiasis, which is a significant cause of morbidity in China and the Philippines. Here we present a draft genomic sequence for the worm. The genome provides a genetic insight into the molecular architecture and host interaction of this complex metazoan pathogen that can exploit host nutrients, neuroendocrine hormones and signalling pathways for growth, development and maturation. Having a complex nervous system and a well-developed sensory system, *S. japonicum* can accept stimulation of the corresponding ligands as a physiological response to different environments, such as fresh water or the tissues of its intermediate and mammalian hosts. Numerous proteases, including cercarial elastase, are implicated in mammalian skin penetration and haemoglobin degradation. The genomic information will serve as a valuable platform to facilitate development of new interventions for schistosomiasis control.

2013



The genomes of four tapeworm species reveal adaptations to parasitism

Isheng J. Tsai,^{1,2*} Magdalena Zarowiecka,^{1*} Nancy Horroy,^{1*} Alejandro Garciarrubio,^{1*} Alejandro Sanchez-Flores,^{1,3} Karen L. Brooks,¹ Alan Tracey,¹ Ranil J. Bubes,¹ Gladys Fragozo,¹ Edita Scutaru,¹ Martin Aslet,¹ Helen Bennett,¹ Jianping Cai,¹ Federico Camicla,¹ Richard Clark,¹ Marcela Cucher,¹ Nishadi De Silva,¹ Tim A. Day,¹ Peter Deplazes,¹ Karel Estrada,¹ Cecilia Fernández,¹ Peter W. H. Holland,¹⁰ Junling Huo,¹ Songjian Hu,¹ Thomas Hackvale,¹ Stacy S. Hung,¹² Laura Kamenetzky,¹ Jacqueline A. Keane,¹ Ferenc Kiss,¹³ Urrel Koziel,¹ Olivia Lambert,¹ Kan Liu,¹⁴ Xuenong Luo,¹ Yingfeng Luo,¹ Natalia Macchiaroli,¹ Sarah Nichol,¹ Jordi Papse,¹ John Parkinson,^{1,17} Natasha Pouchkina-Stantcheva,¹ Niclas Ridderstråle,^{1,13} Mara Rosenzvit,¹ Gustavo Salinas,¹ James D. Watson,¹ Mostafa Zamanian,¹ Yalong Zheng,¹ The *Taenia solium* Genome Consortium,¹ Xuepeng Cai,¹ Xavier Soberón,^{1,14} Peter D. Olson,¹ Juan P. Laclette,¹ Klaus Brehm,¹ and Mathew Berriman¹

2014

FlatDB a south american project

- A regional Project aimed at creating a database on flatworm genomes and transcriptomes (AR;BR;UY)
- Working on trematodes and cestodes
- Build upon SchistoDB

The screenshot shows the SchistoDB homepage from Version 3.0, dated 25 Aug 11. The top navigation bar includes links for Home, New Search, My Strategies, My Basket (0), Tools, Data Summary, Downloads, Community, and a Favorites section. A search bar at the top right allows users to search by Gene ID (Smp_043030) or Gene Text (synth*). A yellow warning box states: "This pre-release version of SchistoDB is available for early community review. Please explore the site and contact us with your feedback. This site is under active development so there may be incomplete or inaccurate data and occasional site outages can be expected." The main content area features three large boxes: "Identify Genes by:" (listing options like Text, IDs, Species, Genomic Position, Gene Attributes, Protein Attributes, Protein Features, Similarity/Pattern, Transcript Expression, Cellular Location, Putative Function, and Evolution), "Identify Other Data Type:" (listing Genomic Sequences, Genomic Segments (DNA Motif), ESTs, and ORFs), and "Tools:" (listing BLAST, Sequence Retrieval, PubMed and Entrez, Genome Browser, and Web Services). On the left sidebar, there are sections for News (with a note about the beta release), Community Resources (with a link to expand for 1 new item), Web Tutorials, and Information and Help (with a link to expand for 9 new items). The footer includes copyright information (SchistoDB 3.0 - August 15, 2011 ©2011 The EuPathDB Project Team), a logo for the Wellcome Trust, and a footer message: "Please Contact Us with any questions or comments".



Unified helminth genomes database

2016

WormBase ParaSite Version: WBPS19 (WS291) - Archive: WBPS18

Search WormBase ParaSite... 

e.g. *O. volvulus*, PRJNA60051, WBGene00262434, Bma-eat-4, eat-4 or metallopeptidase

Genome List BLAST BioMart REST API Downloads Tools WormBase Login Register Help and Documentation

Announcements

Announcing WormBase ParaSite 19 posted 8 months ago by stephbrown28

We are pleased to announce the 19th release of WormBase ParaSite (WBPS19), bringing new and updated genomes, data from RNASeq studies, and additional annotation files for download. WBPS19 hosts 274 different genomes representing 208 distinct species, includes an additional 41 new genome assemblies for 14 existing and 27 new species. Additional Species *Bradyinema listronotus* (PRJNA842945), [read more]

Blog

Announcing WormBase ParaSite 19 posted 8 months ago by stephbrown28

We are pleased to announce the 19th release of WormBase ParaSite (WBPS19), bringing new and updated genomes, data from RNASeq studies, and additional annotation files for download. WBPS19 hosts 274 different genomes representing 208 distinct species, includes an additional 41 new genome assemblies for 14 existing and 27 new species. Additional Species *Bradyinema listronotus* (PRJNA842945), [read more]

Tutorial: Display variants on AlphaFold-predicted 3D protein structures posted 1 year ago by Dionysios Grigoriadis

You've sequenced your samples and identified variants. Great! Now, here's how you can use WormBase ParaSite's new feature to find out the effect of your variants on 3D AlphaFold protein structures and interactions: 2. Click the 'Variant Effect Predictor' button to open the VEP web tool and enter your input data using instructions in the [read more]

About archive sites posted 3 years ago by Faye Rodgers

We're pleased to announce that we have introduced an archiving service. From release 16 onwards, older WormBase ParaSite releases will remain available for browsing. We have introduced this service to help users in transitions between genome and annotation versions. Older, draft assemblies are increasingly being superseded by highly contiguous assemblies generated with modern sequencing technologies. [read more]

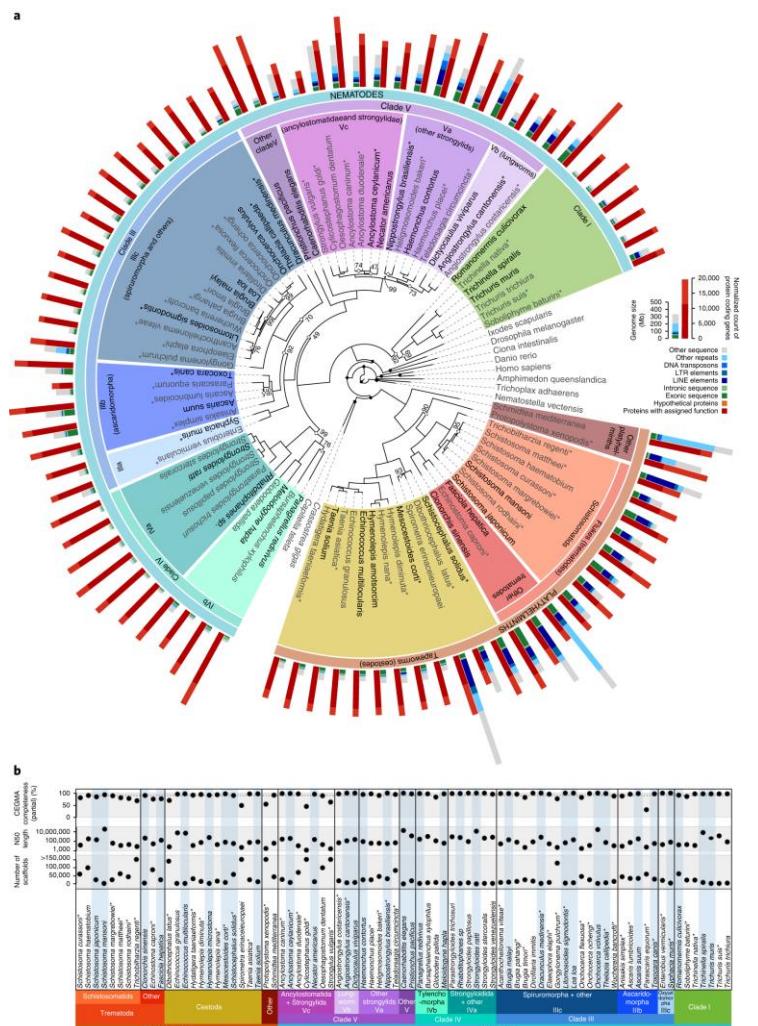
Find a genome

[+] Nematoda (Roundworms)

[+] Platyhelminthes (Flatworms)

Statistics

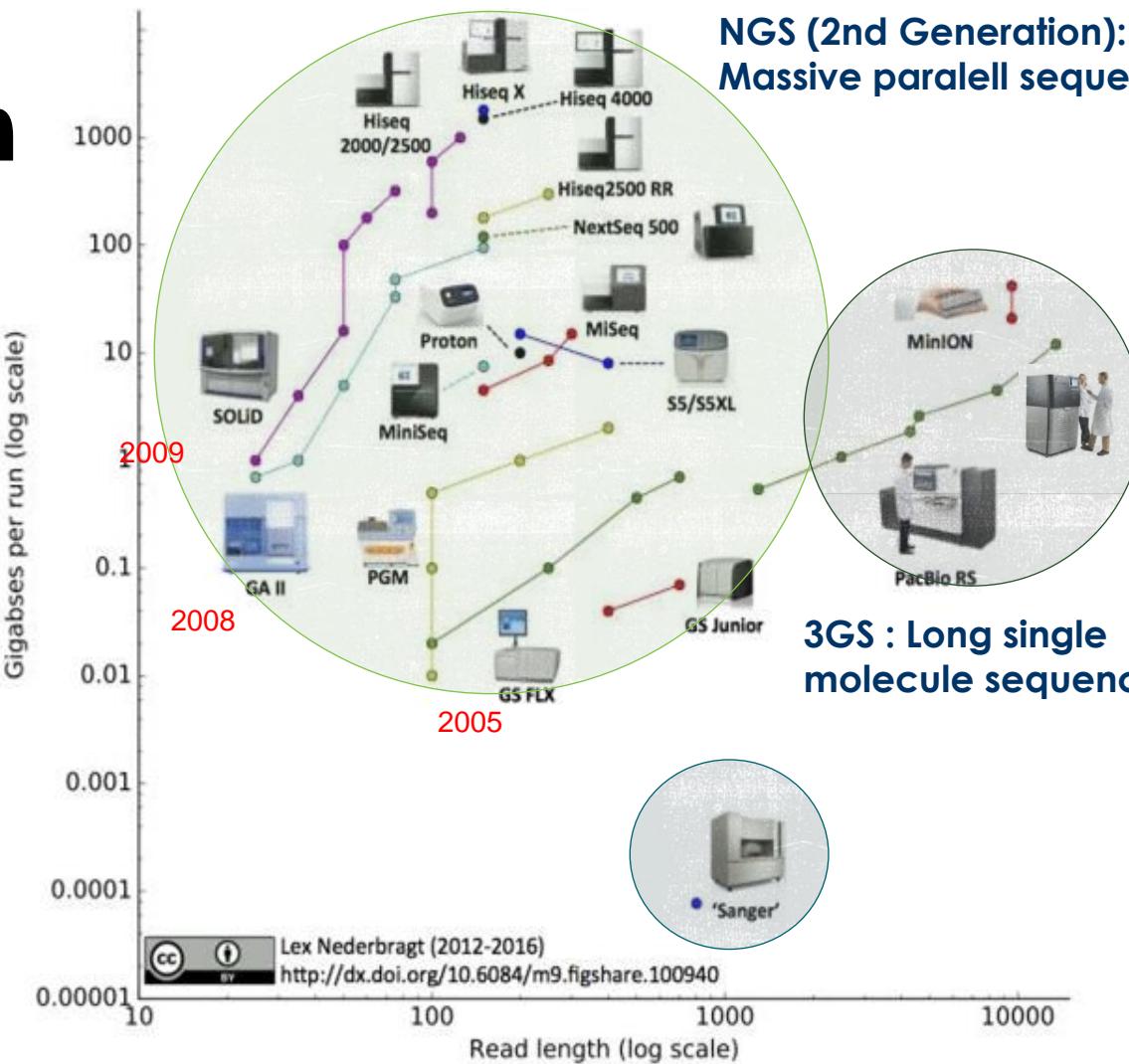
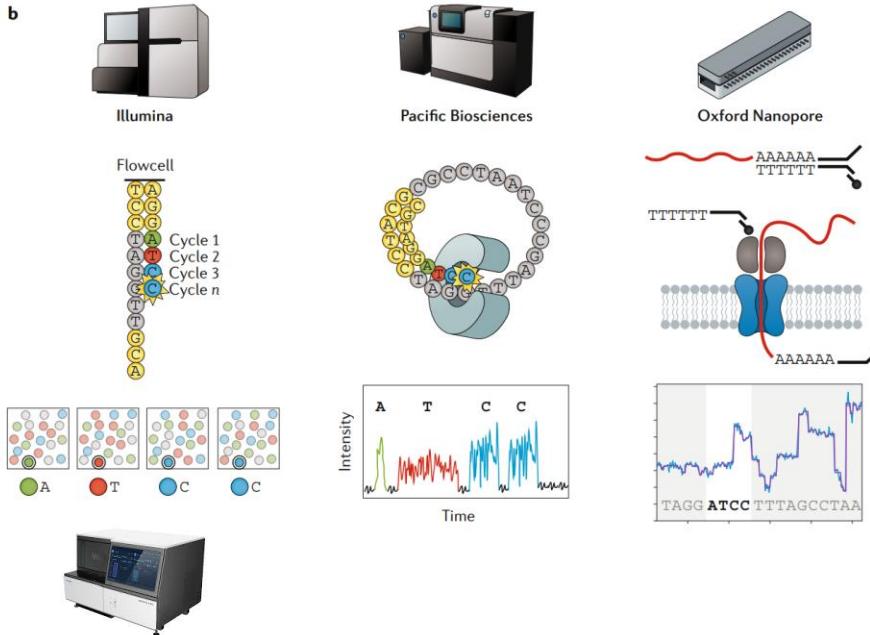
- Version: WBPS19 (March 2024)
- WormBase Version: WS291
- 274 genomes, representing 208 species



International Helminth Genomes Consortium. Comparative genomics of the major parasitic worms.
Nat Genet 51, 163–174 (2019). <https://doi.org/10.1038/s41588-018-0262-1>

Sequencing Technologies evolution

b

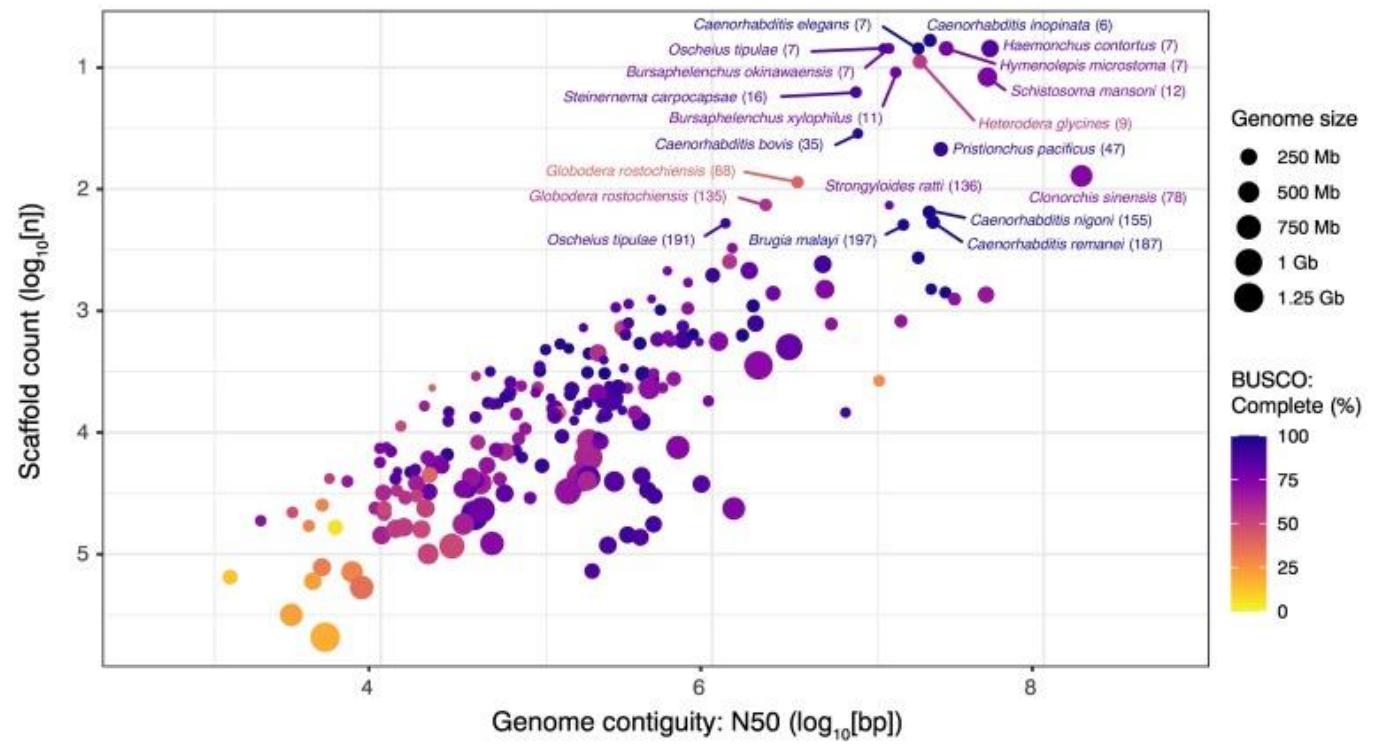
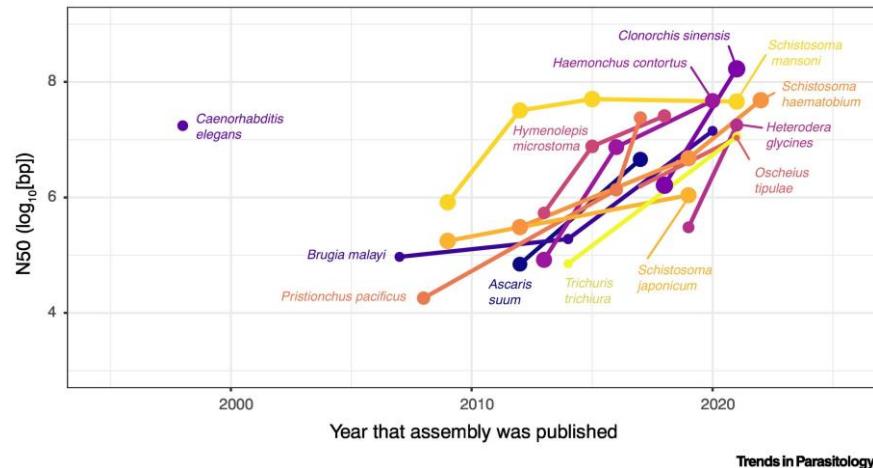


NGS (2nd Generation):
Massive parallel sequencing



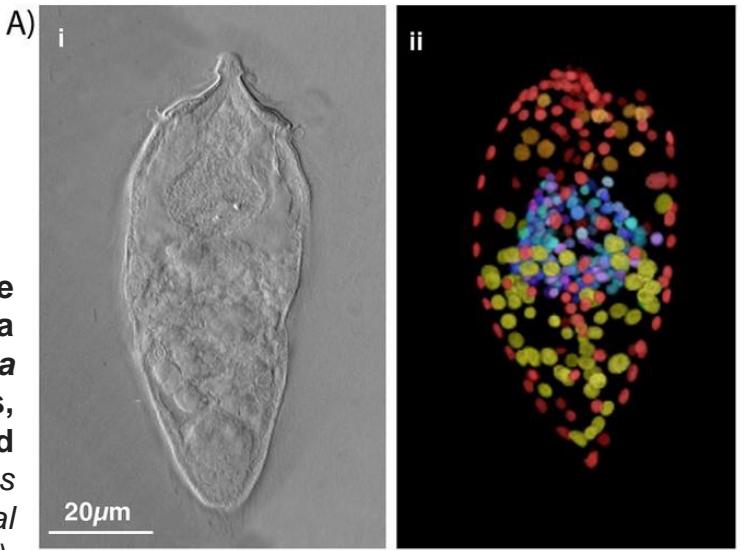
Improved genome quality

- Chromosome level assemblies
- Repetitive nature of genomes
- Sintenny and genome evolution
- Intraspecific variation



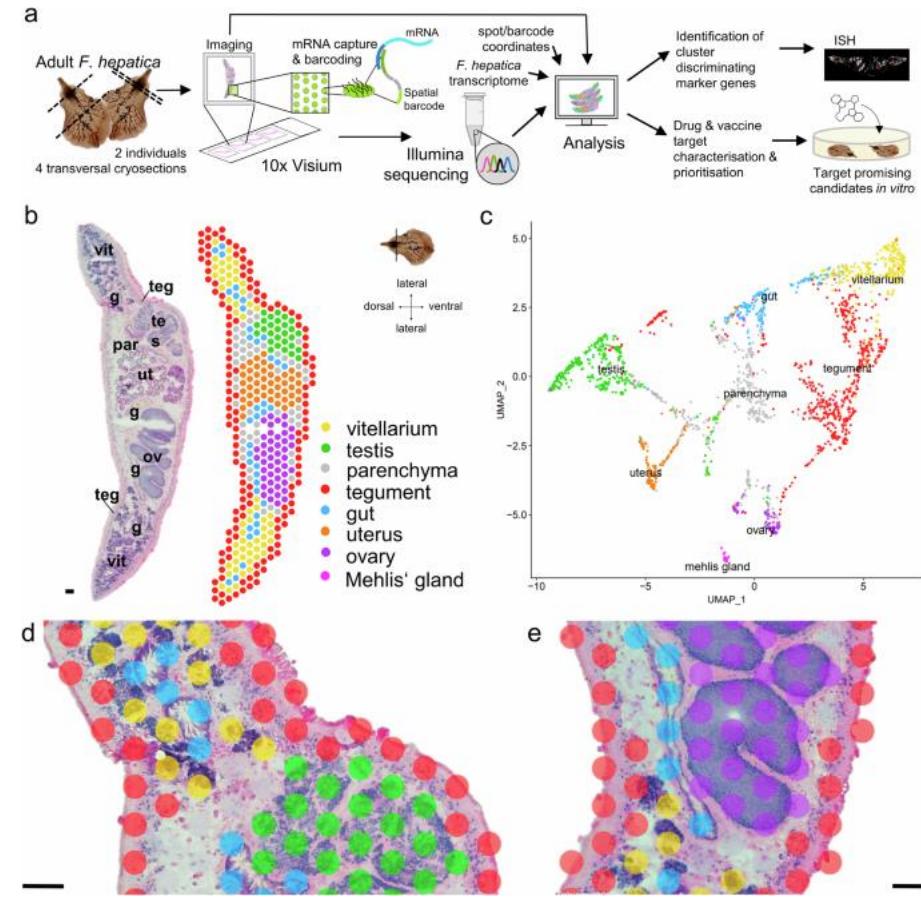
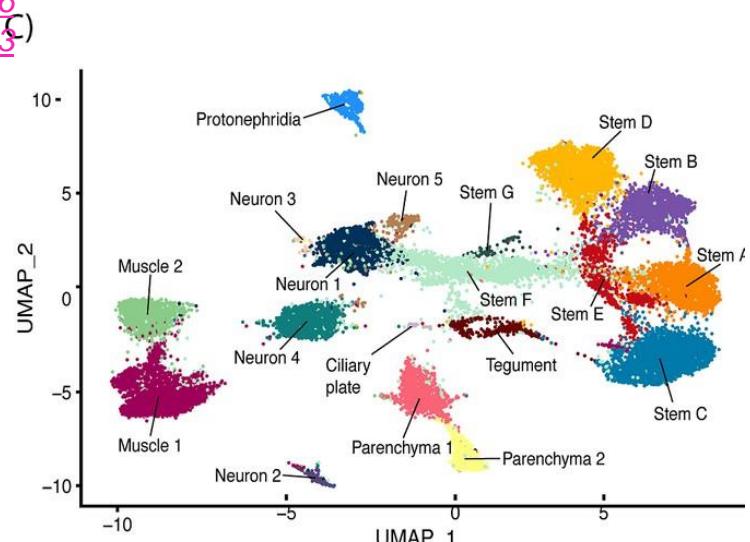
Improving helminth genome resources in the post-genomic era,
S. Doyle Trends in Parasitology, Volume 38, Issue 10, 831 - 840
DOI: [10.1016/j.pt.2022.06.002](https://doi.org/10.1016/j.pt.2022.06.002)

Transcriptomics new paths



A single-cell atlas of the miracidium larva of *Schistosoma mansoni* reveals cell types, developmental pathways, and tissue architecture Tess Attenborough et al *eLife* (2024).

<https://doi.org/10.7554/eLife.95628>

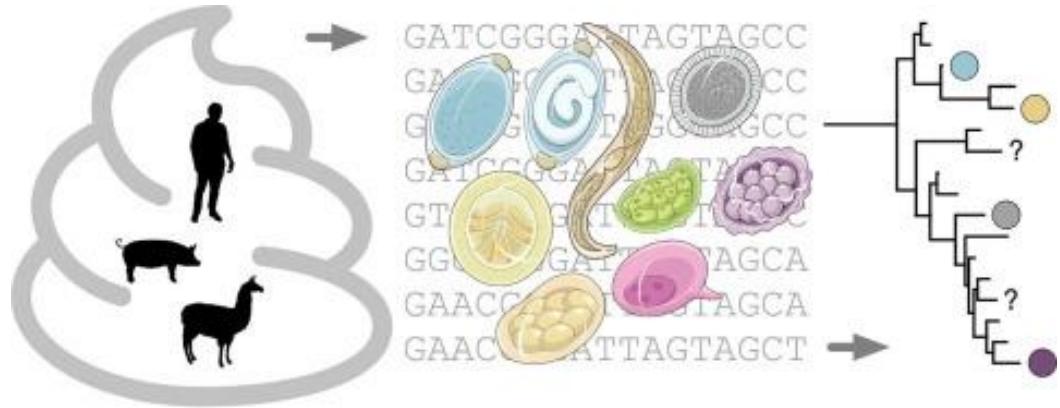


Spatial transcriptomics of a parasitic flatworm provides a molecular map of drug targets and drug resistance genes. Svenja Gramberg et al

Nature Communications (2024)

/10.1038/s41467-024-53215-3

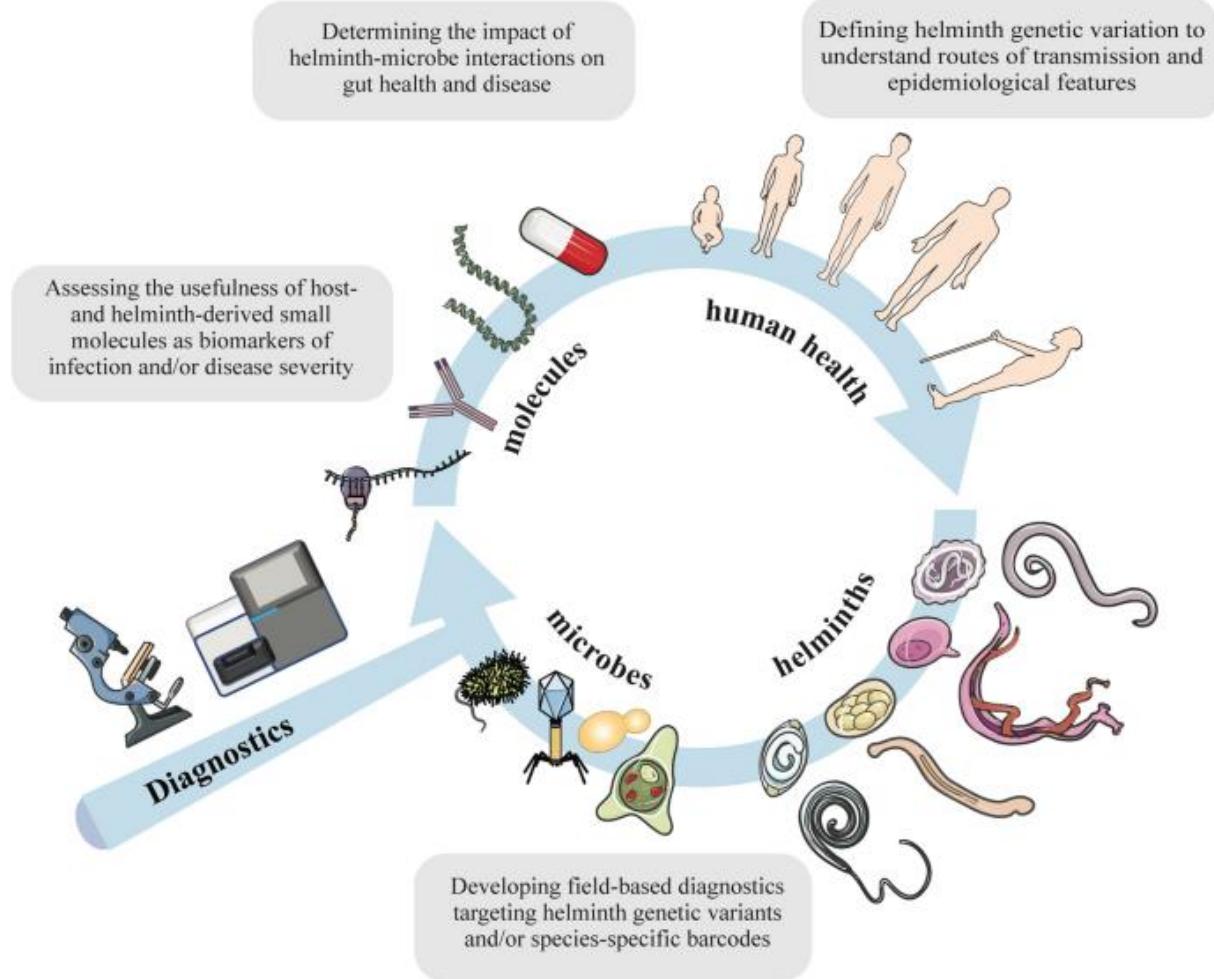
Parasites in communities



Helminth egg images from Sanger Medical Art (<https://www.sanger.ac.uk>) used under Creative Commons Attribution 3.0 Unported License

Evaluation of genome skimming to detect and characterise human and livestock helminths . M. Papaiakovou et al. *Int J Parasitol* (2023)

[DOI /10.1016/j.ijpara.2022.12.002](https://doi.org/10.1016/j.ijpara.2022.12.002)



Worms and bugs of the gut: the search for diagnostic signatures using barcoding, and metagenomics–metabolomics

M. Papaiakovou et al. *Parasites & Vectors* (2022)

[DOI/10.1186/s13071-022-05225-7](https://doi.org/10.1186/s13071-022-05225-7)



Helminth Bioinformatics - Latin America & the Caribbean

18–24 May 2025

Universidad de la Republica, Uruguay

Timetable

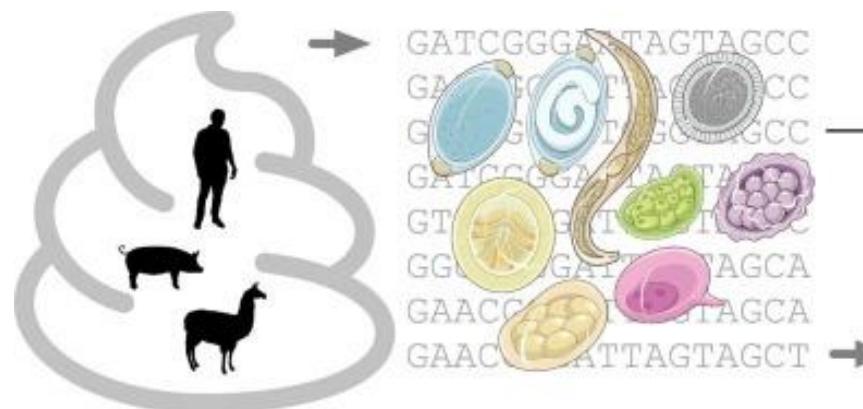
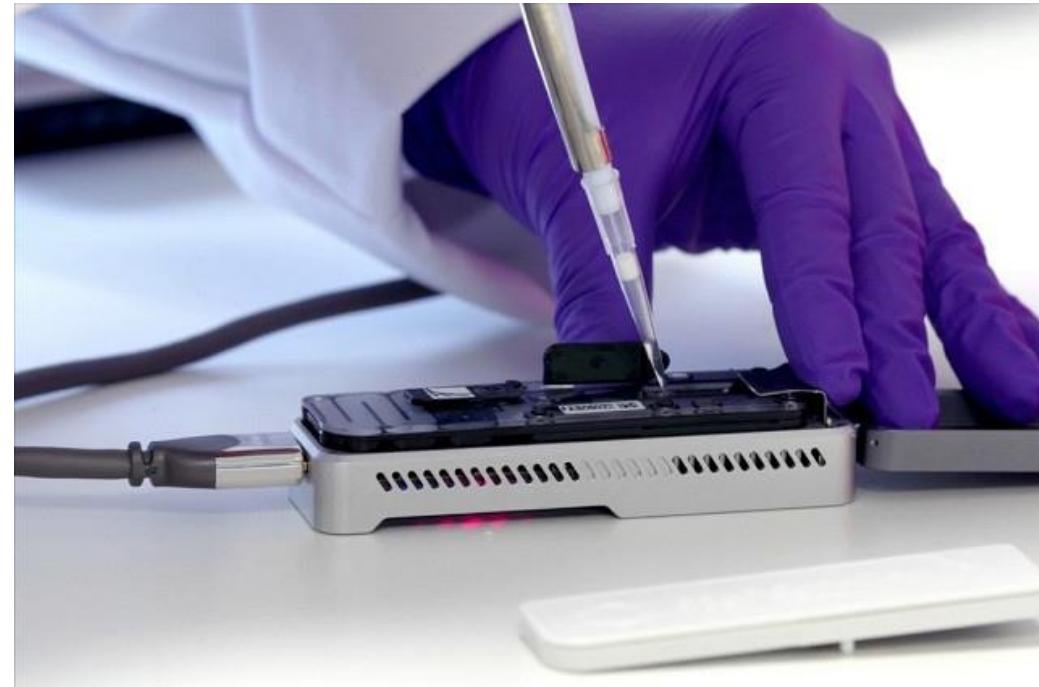
with novelties...

Helminth Bioinformatics, 18 - 24 May 2025, Montevideo - Uruguay							UNIVERSIDAD DE LA REPÚBLICA URUGUAY
Sunday 18 May	Monday 19 May	Tuesday 20 May	Wednesday 21 May	Thursday 22 May	Friday 23 May	Saturday 24 May	
8:00 - 9:00	Transport to Institute	Transport to Institute	Transport to Institute	Transport to Institute	Transport to Institute		
9:00 - 10:00	Oxford Nanopore Sequencing Setup Lecture	Assembly (practical) Agustín Baricalla	WormBase ParaSite2 : Tools & Biomart Pepe Tort	Transcriptomics: Mapping Anna Protasio	Genetic Diversity: Mapping Marina Papalakou		8:00 - 9:00
10:00 - 11:00	Oxford Nanopore library prep Laura Kamenetzky						
11:00 - 12:00	Break	Break	Break	Break	Break		
12:00 - 13:00	Registration & Lunch	Oxford Nanopore library prep Laura Kamenetzky	Mitochondrial Annotation Santiago Fontenla	Apollo Setup and Exploration; Community Annotation Matt Benman	Transcriptomics: Differential Expression Anna Protasio	Genetic Diversity: SNP Calling & VEP Marina Papalakou	
13:00 - 14:00	Introductions: Wellcome Connecting Science Universidad de la República Training Team Participants	LUNCH	LUNCH	LUNCH	LUNCH	LUNCH	13:00 - 14:00
14:00 - 15:00		Assembly (lecture) Agustín Baricalla	WormBase ParaSite: Basics Pepe Tort	Comparative Genomics and Apollo	GO term. enrichment Anna Protasio	Mitogenomics: Phylogenomics Andrés Irarate	14:00 - 15:00
15:00 - 16:00	Break	Assembly (practical) Agustín Baricalla	Break	Break	Break	Wrap-up + Action Planning Break & End of course	15:00 - 16:00
16:00 - 17:00	Advanced Learning Skills	Unix Refresher Steve Doyle	WormBase Parasite: Basics cont. Pepe Tort	R refresher Steve Doyle	Single cell Santiago Fontenla	Transport to Hotel	16:00 - 17:00
17:00 - 18:00	Public Engagement			Transport to Hotel			17:00 - 18:00
18:00 - 19:00	Networking Drinks			break at hotel			18:00 - 19:00
19:00 - 21:00	Welcome Dinner			Public Engagement Part 2 & Dinner			19:00 - 21:00
	Sunday 18 May	Monday 19 May	Tuesday 20 May	Wednesday 21 May	Thursday 22 May	Friday 23 May	Saturday 24 May



First wet lab experience...

- Generating your own data (genome skimming)
- Analyzing it



Helminth egg images from Servier Medical Art (<https://smart.servier.com>) used under Creative Commons Attribution 3.0 Unported License

Helminth Bioinformatics	
Monday 19 May	Tuesday 20 May
Transport to Institute	Transport to Institute
Oxford Nanopore Sequencing Setup Lecture	
Oxford Nanopore library prep Laura Kamenetzky	Assembly (practical) Agustín Baricalla
Break	Break
Oxford Nanopore library prep Laura Kamenetzky	Mitochondrial Annotation Santiago Fontenla
Seminar: Molecular epidemiology of helminths (and genomics of <i>Spirocerca lupi</i>) Alicia Rojas, UCR , CR	Proteogenomics of Clade I Nematodes: The Case of the Giant Kidney Worm Gisela Franchini, UNLP, AR
LUNCH	LUNCH
Assembly (lecture) Agustín Baricalla	WormBase ParaSite: Basics Pepe Tort
Assembly (practical) Agustín Baricalla	Break
Unix Refresher Steve Doyle	WormBase Parasite: Basics cont. Pepe Tort
Transport to Hotel	Transport to Hotel
Monday 19 May	Tuesday 20 May



Genome Databases & Curation ...

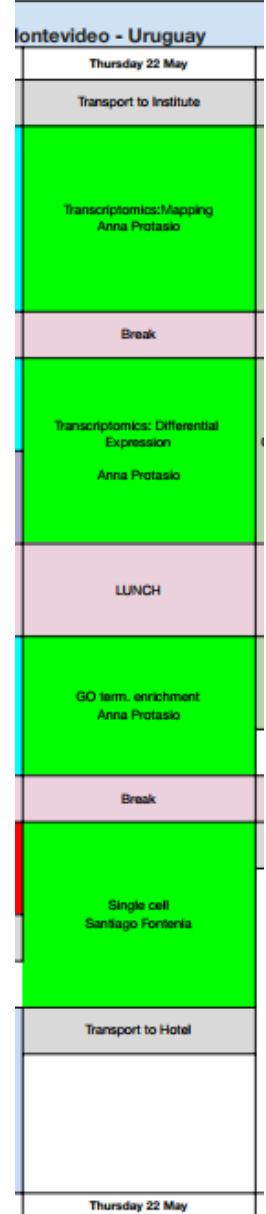
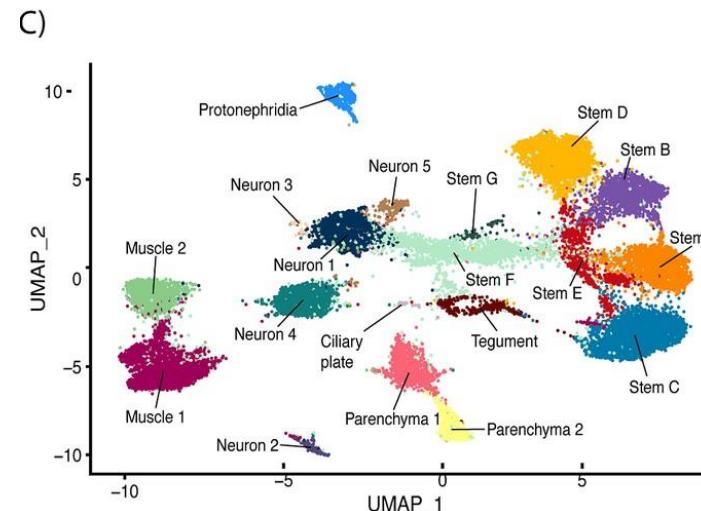
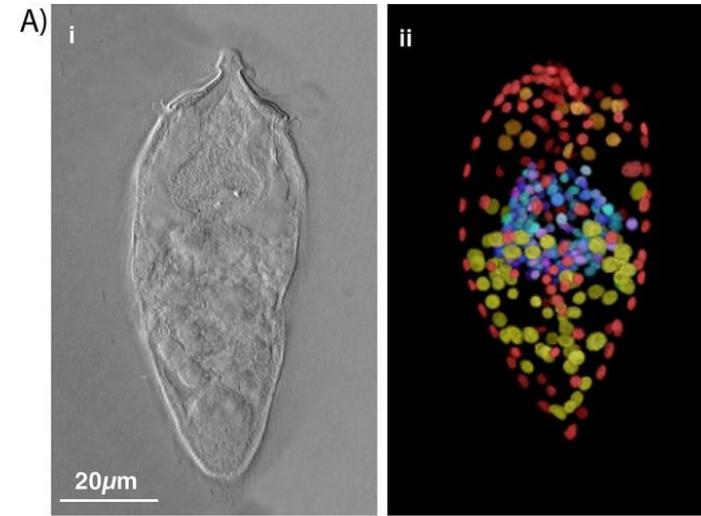
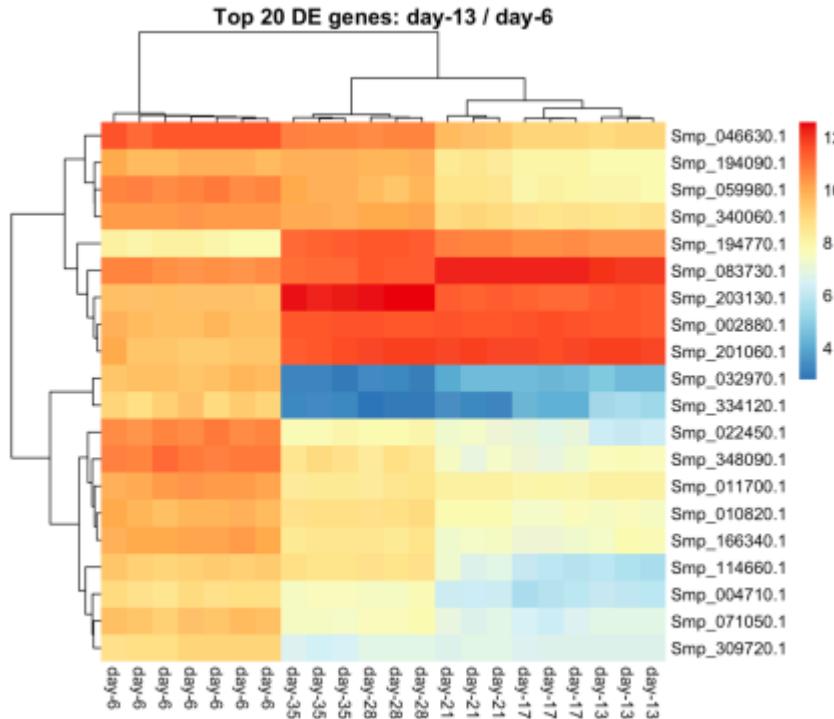
- Working with WBPS
- Introducing Apollo,
 - “editing & curating your genome”

The image is a composite of two parts. On the left, there is a screenshot of the Apollo gene curation software. The interface shows a genomic track for the gene TMU_001_pileup, with various evidence tracks like Illumina coverage, Isoseq reads, and RNA-seq. On the right, there is a photograph of a white rocket launching from a launch pad, with a bright plume of smoke and fire at its base.

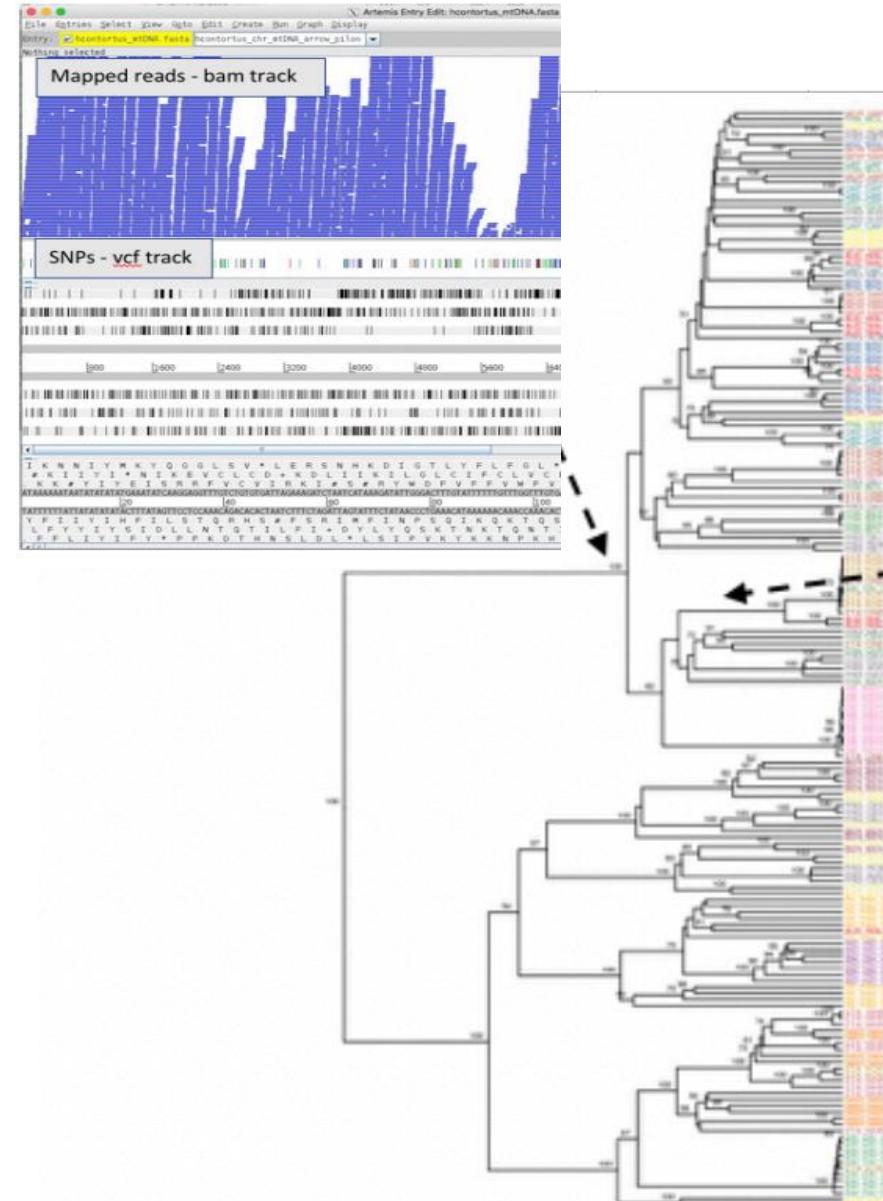
Helminth Bioinformatics, 18 - 24 May 2025, N	
Tuesday 20 May	Wednesday 21 May
Transport to Institute	Transport to Institute
Assembly (practical) Agustín Barcala	WormBase ParaSite2 : Tools & Biomart Pepe Tort
Break	Break
Mitochondrial Annotation Santiago Fontenla	Apollo Setup and Exploration, Community Annotation Matt Berniman
Proteogenomics of Clade I Nematodes: The Case of the Giant Kidney Worm Gisela Franchini, UNLP, AR	Seminar : Insights into cestode development Uriel Koziel, UdeA-R, UY
LUNCH	LUNCH
WormBase ParaSite: Basics Pepe Tort	Comparative Genomics and Apollo
Break	Break
WormBase Parasite: Basics cont. Pepe Tort	R refresher Steve Doyle
Transport to Hotel	Transport to Hotel
break at hotel	
Transport to Hotel	Public Engagement Part 2 & Dinner
Tuesday 20 May	Wednesday 21 May



Gene expression bulk and ... single cell ...



Mapping, variation & phylogenetics



Friday 23 May
Transport to Institute
Genetic Diversity: Mapping Marina Papalakou
Break
Genetic Diversity: SNP Calling & VEP Marina Papalakou
LUNCH
Mitogenomics: Phylogenomics Andres Iriarte
Wrap-up + Action Planning
Break & End of course
Transport to Hotel
Friday 23 May

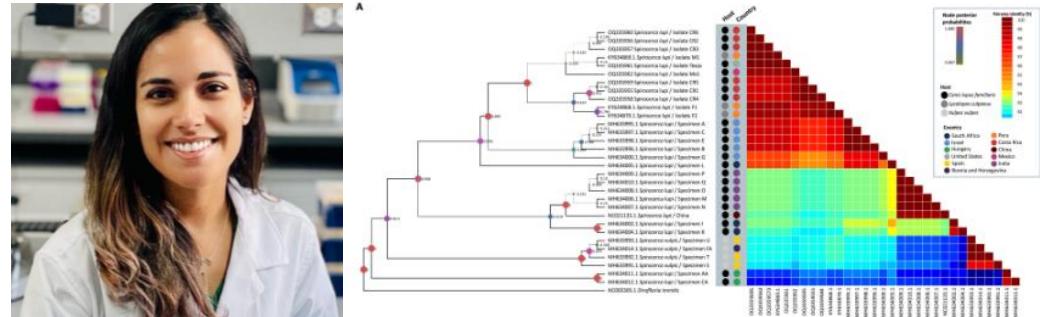


Conferences

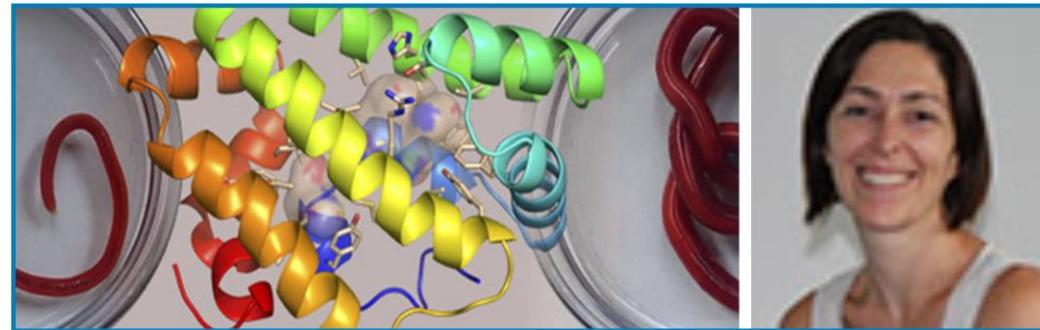
Alicia ROJAS

UCR

Parasite Epidemiology



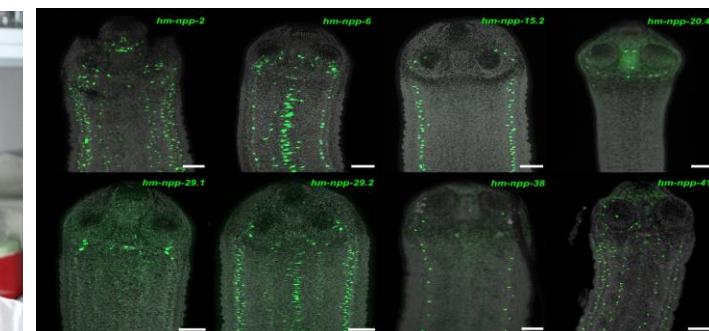
Gisela FRANCHINI UNLP Proteogenomics



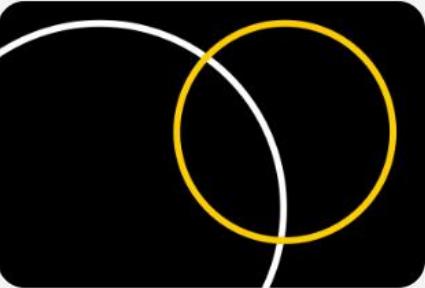
Uriel KOZIOL

UdelaR

Parasite Development



**Wellcome Connecting Science's mission
is to enable everyone to explore genomic
science and its impact on research,
health and society.**



About us



Public Engagement



Learning



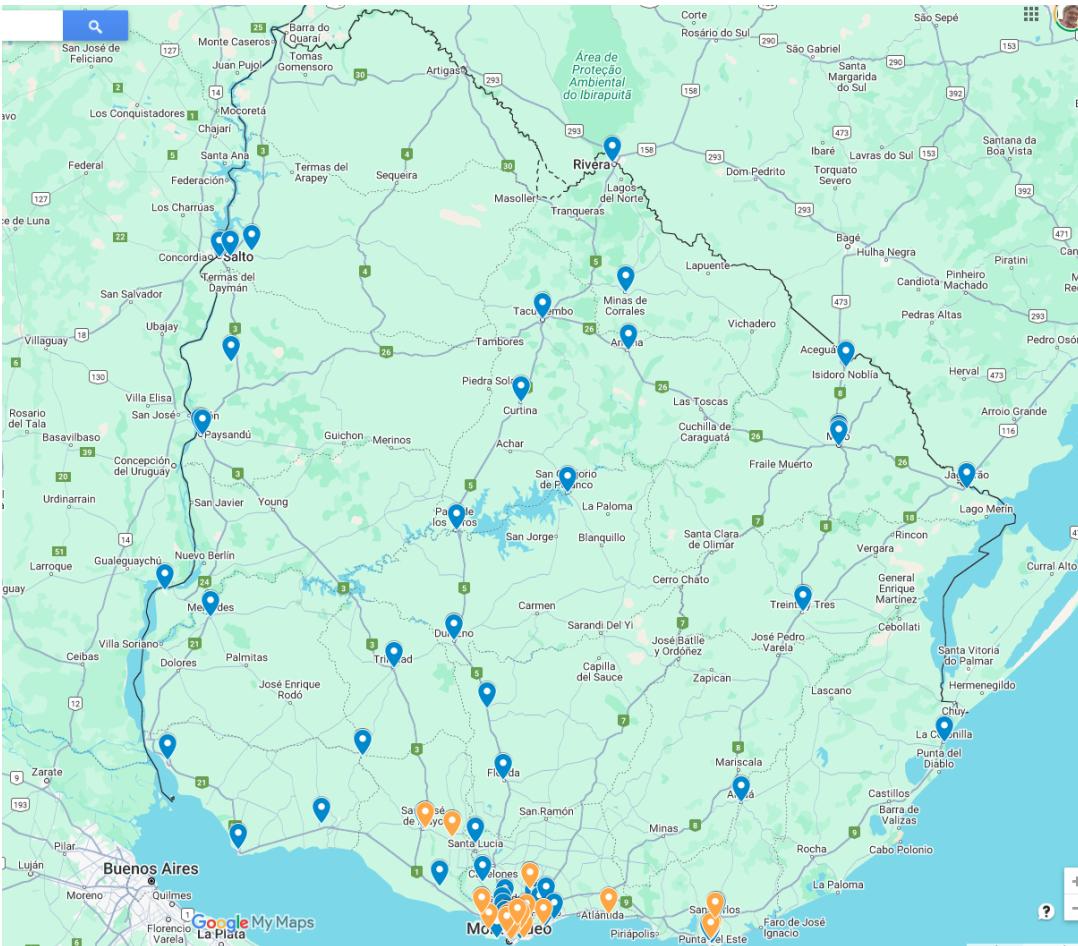
Public programmes



Research and society



Workshop with Secondary teachers



Cuando: Sábado 24 de mayo de 2025, de 10.00 a 15.00 hrs.

Dónde: Instituto de Higiene, Montevideo.

Este evento está abierto a profesores de biología de educación secundaria de todo el país.

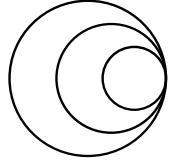
Este evento es gratuito para todos los educadores participantes.

Aportar a la enseñanza de las ciencias en instituciones educativas locales y a concientizar sobre las carreras científicas, para formar los futuros investigadores genómicos del Uruguay.



Ministerio
de Educación y Cultura

Declarado
de Interés Ministerial



wellcome
connecting
science

thanks!

