

# Comparative genomics of parasitic helminths

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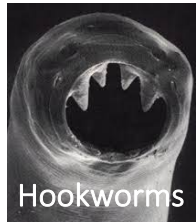
LSHTM Pathogen Genomics

# Overview



- Comparative genomics of the major parasitic worms
- Evolutionary insight using chromosome-scale genomes
- Shared parasite variation sheds light on adaption and migration

# Comparative genomics of the major parasitic worms



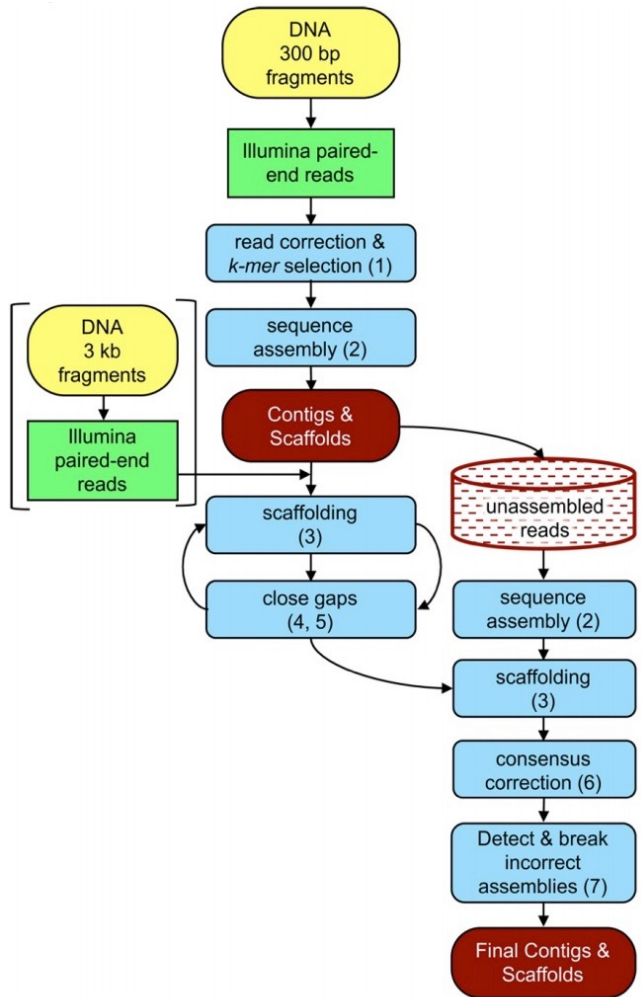
- Helminths represent a significant health and economic burdens on humans
- (arguably) genomics has revolutionised our understanding of helminth biology



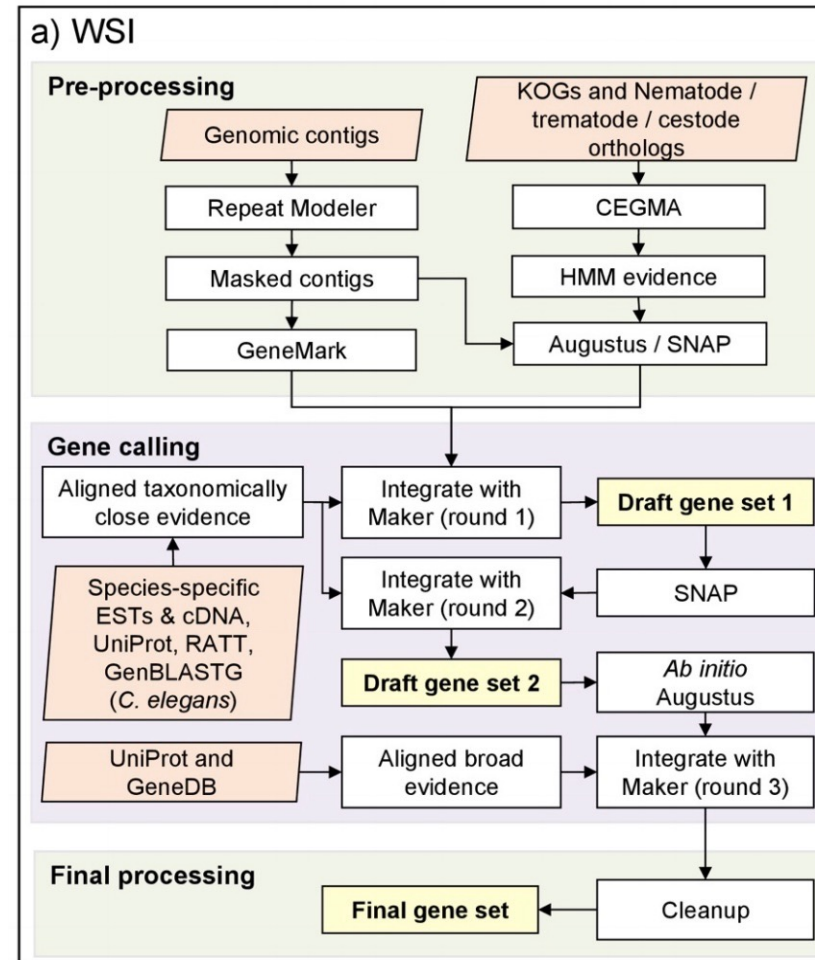
1. To generate ***draft*** genome assemblies for:

2. (Try to) ensure similar sequencing, assembly and annotation approaches for each genome so they are truly **comparable**

# Comparative genomics of the major parasitic worms



Genome assembly

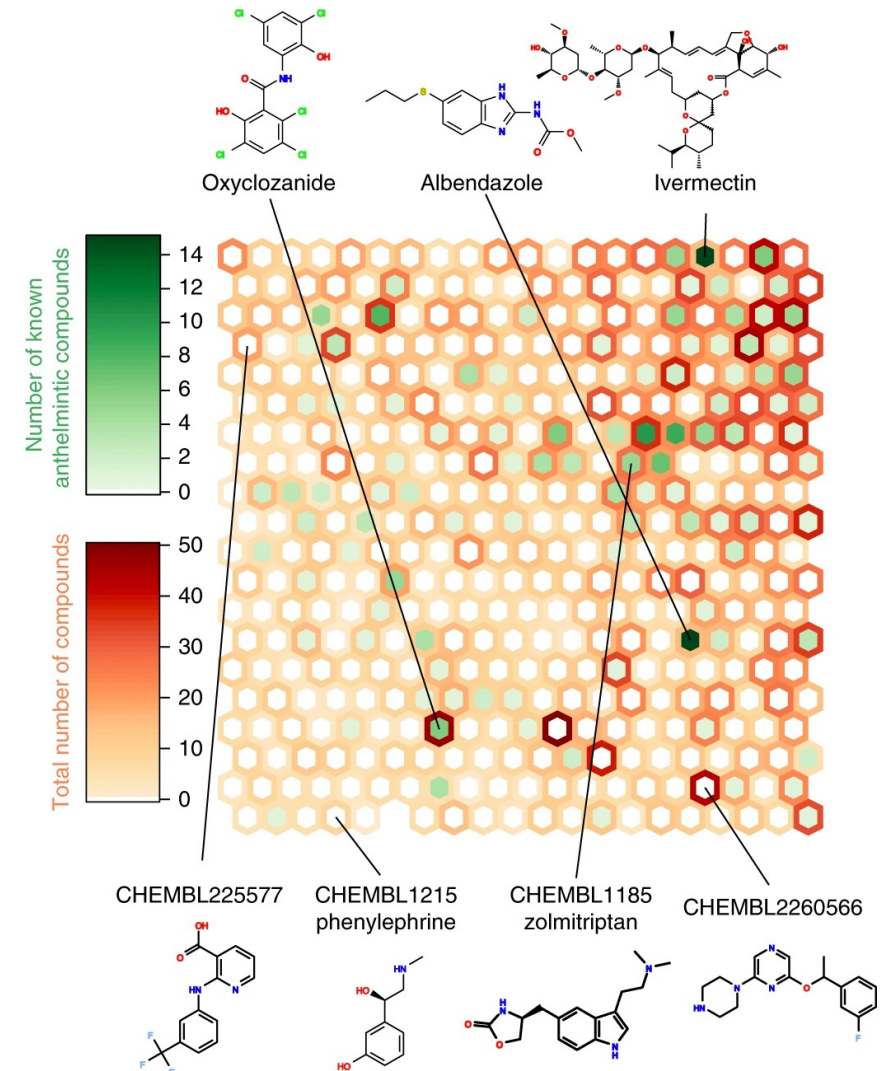


Genome annotation



# Comparative genomics of the major parasitic worms

- Genome size
  - 42 to 700Mb in nematodes
  - 104 to 1,259Mb in platyhelminths.
- Genome content
  - >1.2 million protein coding genes
  - Highlights presence, absence, and expansions of gene families
- Highly conserved pathways
  - Important for interactions with environment, including host
  - Candidate drug targets ->



# Comparative genomics of the major parasitic worms

## WormBase ParaSite

Version: WBPS15 (WS276)

Genome List BLAST BioMart REST API Downloads Tools WormBase

Search WormBase ParaSite...  
e.g. *O. volvulus*, PRJNA60051, WBGene00262434, Bma-eat-4, eat-4 or metalloproteinase

Login Register Help and Documentation

Genomes  
🔗

BLAST  
🔍

BioMart  
📄

API  
📡

Downloads  
⬇️

WormBase  
🐛

Find a genome

[+] Nematoda (Roundworms)

[+] Platyhelminthes (Flatworms)

Statistics

- Version: WBPS15 (October 2020)
- WormBase Version: WS276
- 197 genomes, representing 161 species

### Announcements

#### Announcing WormBase ParaSite Release 15

posted 5 months ago by [Faye Rodgers](#)

We're delighted to announce the release of WormBase ParaSite 15, our biggest release yet! New genomes This release sees the addition of assemblies of 19 new species: 5 *Panagrolaimus*/*Propanagrolaimus* species, including the Antarctic nematode *Panagrolaimus davidi*, from Schiffer et al., 2019. 10 new *Caenorhabditis* species from Stevens et al., 2019 and Stevens et al, 2020. [\[read more\]](#)

#### Alternative gene set for *Necator americanus*

posted 6 months ago by [Faye Rodgers](#)

Logan et al. (2020) have published an alternative set of gene predictions for *Necator americanus* in PLoS Neglected Tropical Diseases, based on both RNA-seq and proteomics data and generated via the MAKER pipeline. Their gene predictions can be downloaded from the WormBase ParaSite FTP site at: [ftp://ftp.ebi.ac.uk/pub/databases/wormbase/parasite/datasets/logan\\_2020\\_32453752](ftp://ftp.ebi.ac.uk/pub/databases/wormbase/parasite/datasets/logan_2020_32453752) Thanks to Javier Sotillo Gallego for providing the data!

### Blog

#### WormBase ParaSite is recruiting

posted 5 months ago by [Faye Rodgers](#)

We're looking for a bioinformatician to join the WormBase ParaSite team. If you have an MSc/PhD in bioinformatics (or related), experience working with relational database systems and an interest in genomics, please consider applying! Informal enquiries to [parasite-help@sanger.ac.uk](mailto:parasite-help@sanger.ac.uk) are welcome. Closing date 23rd November. To apply: <https://www.embl.de/jobs/search/jobs/index.php?ref=EBI01718>

#### On identifiers from external databases and past releases

posted 2 years ago by [Wojtek Bazant](#)

(updated in WBPS13 to reflect archiving functionality and mention gene IDs in GFF dumps) As sequencing projects progress and yield improved data, we occasionally update genomes on the site to provide the best resources available. An example of this is *Schistosoma mansoni*, released in WBPS11. The authors of the new *S. mansoni* annotation preserved identifiers [\[read more\]](#)

#### Genomes we don't have in WormBase ParaSite

posted 2 years ago by [Wojtek Bazant](#)

The work on the version 11 of WormBase ParaSite is ongoing! We now have a list of assemblies of new species, and improved genomes of existing species, that we plan to publish. As well as including data submitted to us directly, we also surveyed the archives and have made an effort to include all assemblies [\[read more\]](#)

[\[Older\]](#)

### Twitter


Tweets by @WBParaSite

WormBase ParaSite Retweeted

**Wellcome Connecting Science C**  
@ACSCevents

Applications closing for #Helminth2021  
Gain hands-on training in #helminth genome analysis.  
Learn read mapping, #transcriptomics & genetic variation analysis, all tailored to address the challenges presented by large helminth genomes.

Apply by 08 Apr :[bit.ly/3fmy6wm](https://bit.ly/3fmy6wm)

 virtual course  
helminth  
bioinformatics  
June 20 - 02 July 2021

Apply by: 08 April 2021

29 Mar 2021

WormBase ParaSite Retweeted

**Thomas D. Otto**  
@Biotofnl

PL RT: More spaces for the African  
Advanced #Bioinformatics #workshop:  
[forms.gle/UjbGwATicEzQQZ...](https://forms.gle/UjbGwATicEzQQZ...)! Free,  
virtual, register until 14/04/2021.  
Need experience in bioinformatics and  
work in Africa.

[Embed](#) [View on Twitter](#)



- *Haemonchus contortus*



# *Haemonchus contortus*: a major pathogen of ruminants

- found worldwide in wild and domesticated ruminants

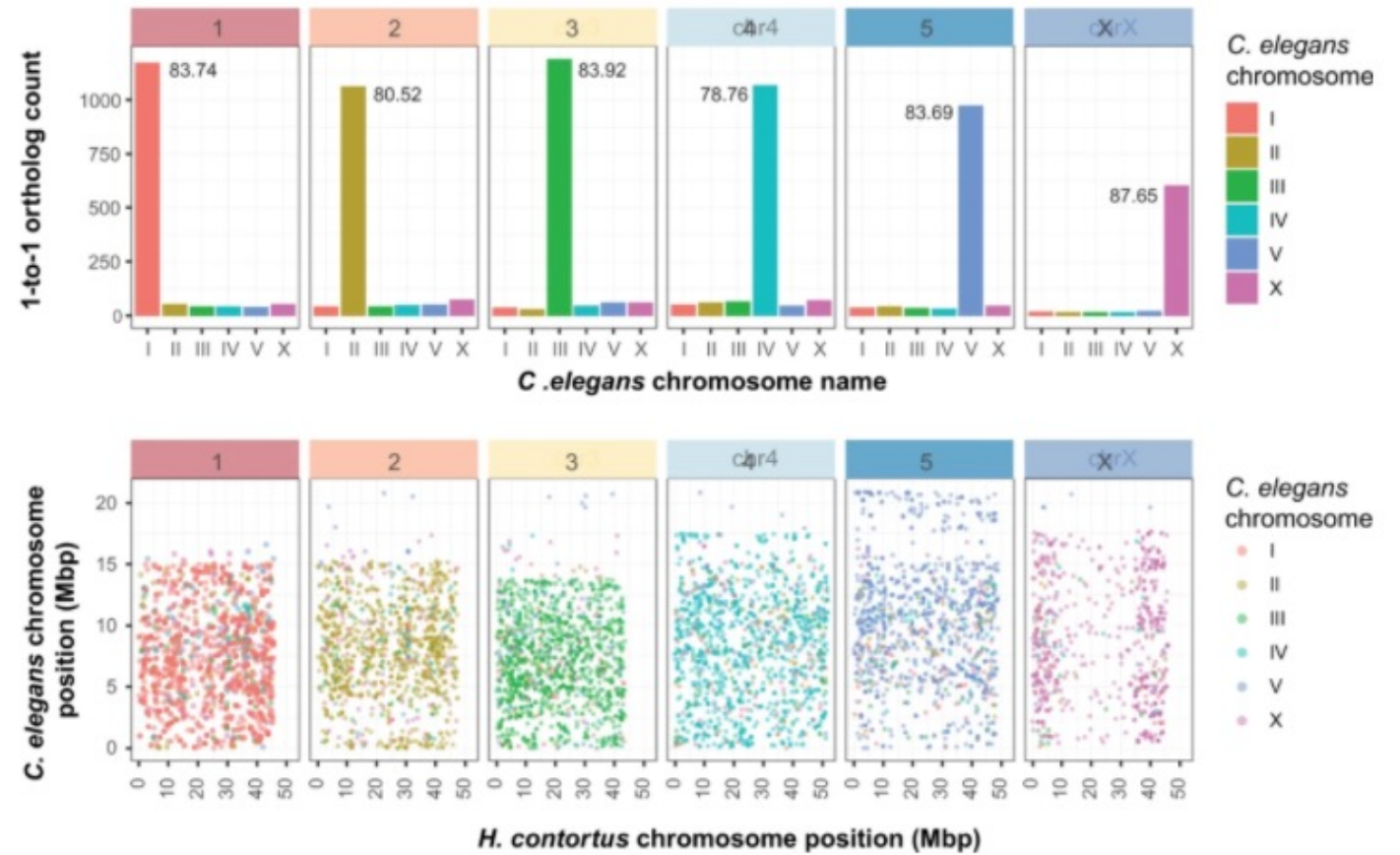
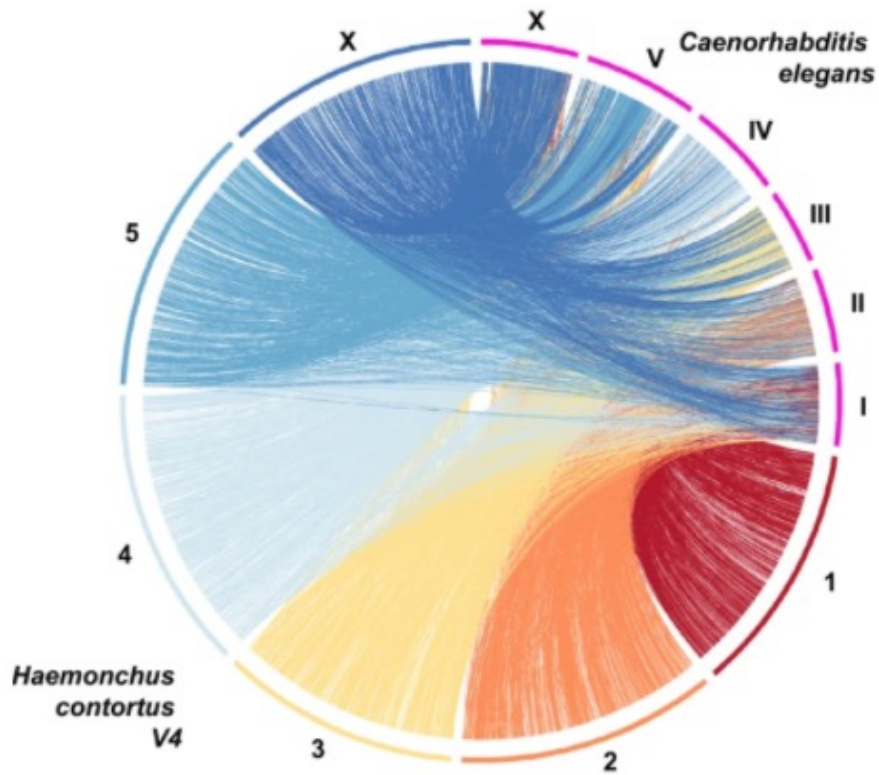


- Adult worms inhabit the abomasum, and feed on blood



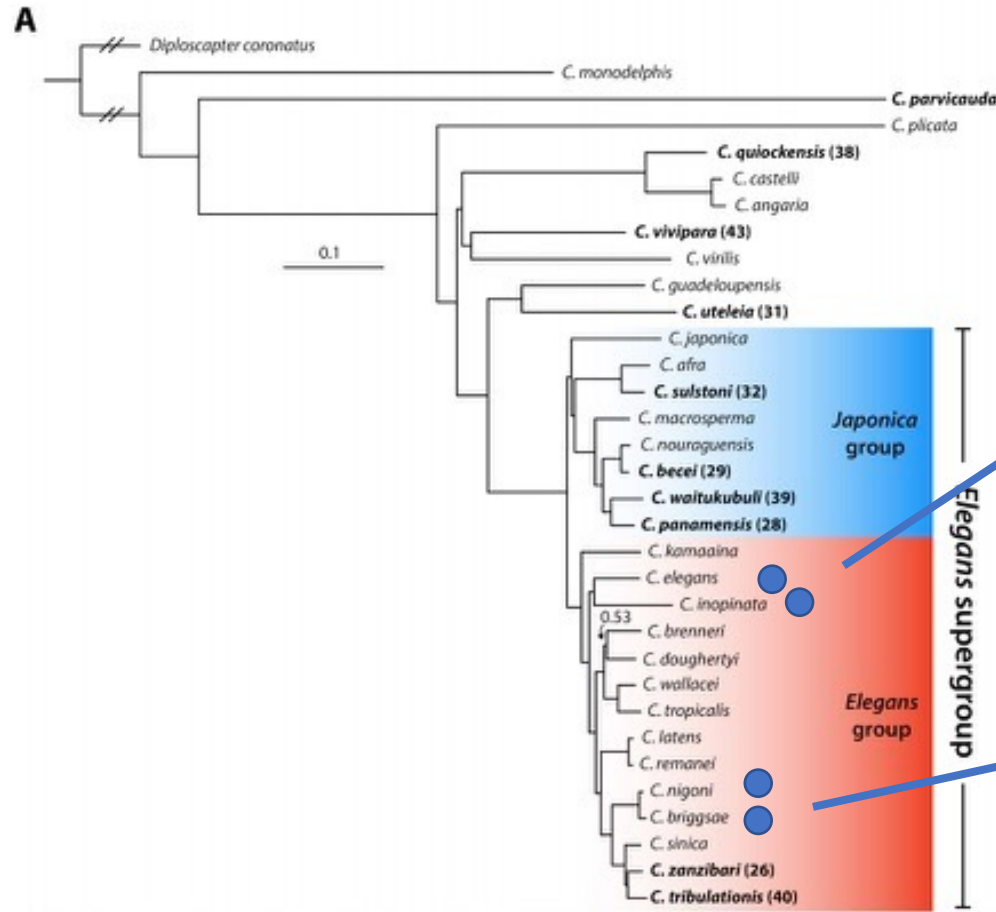
- Drug resistance is common (very high frequency in some regions), including all major classes of anthelmintics

# Evolutionary insight using chromosome-scale genomes

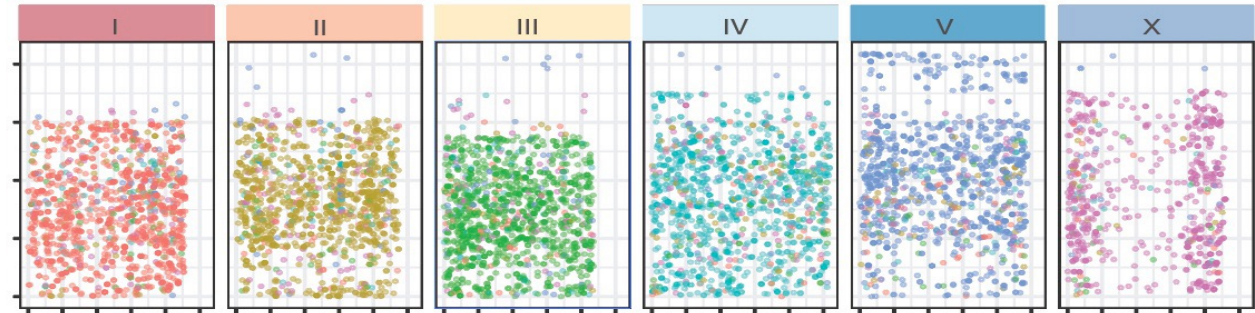




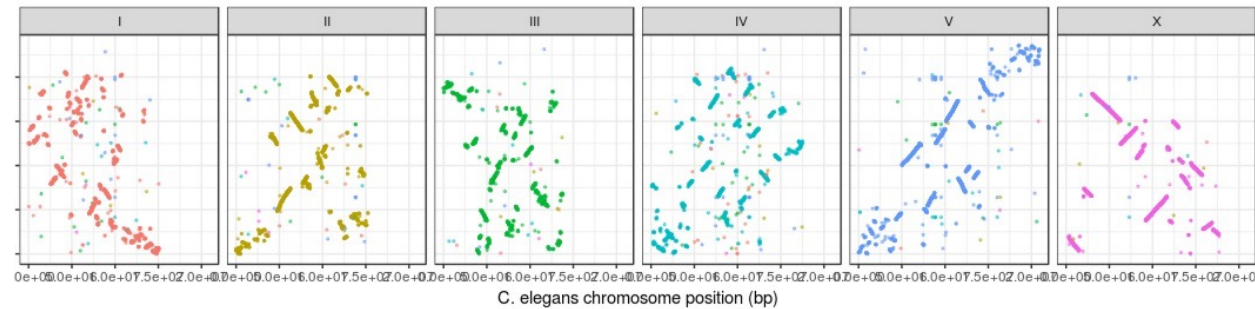
# Evolutionary insight using chromosome-scale genomes



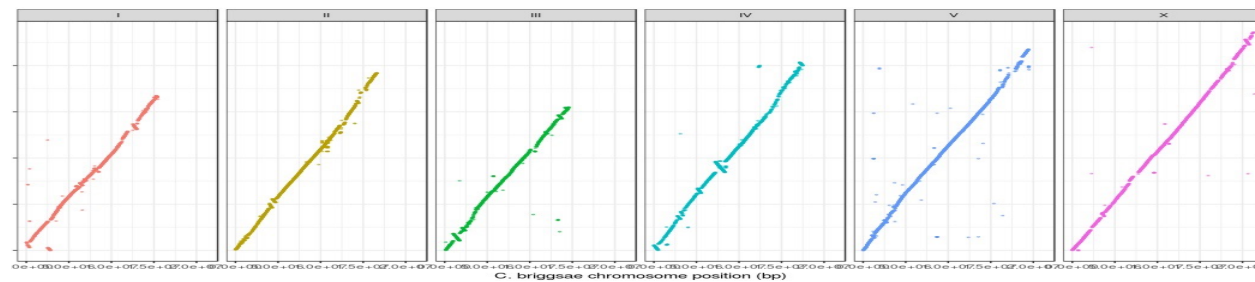
*H. contortus* vs *C. elegans*



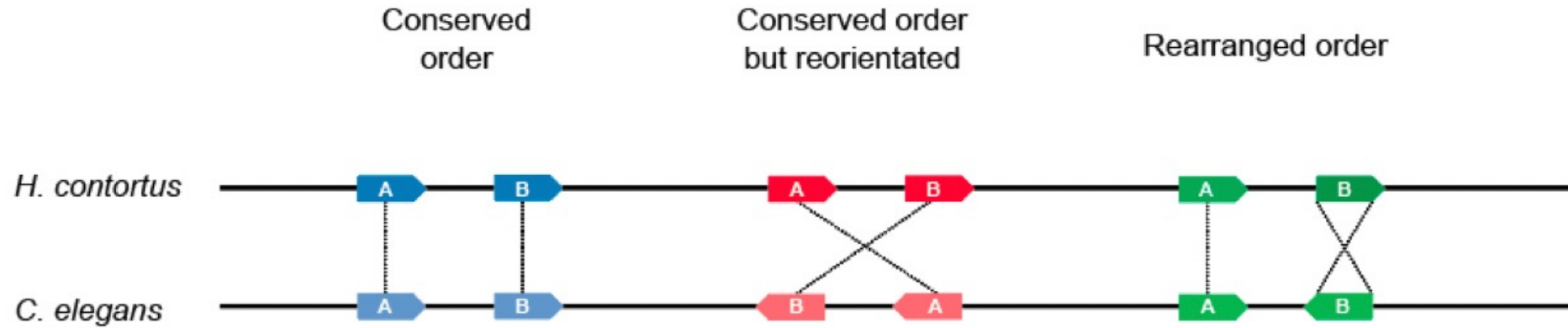
*C. elegans* vs *C. inopinata*



*C. nigoni* vs *C. briggsae*

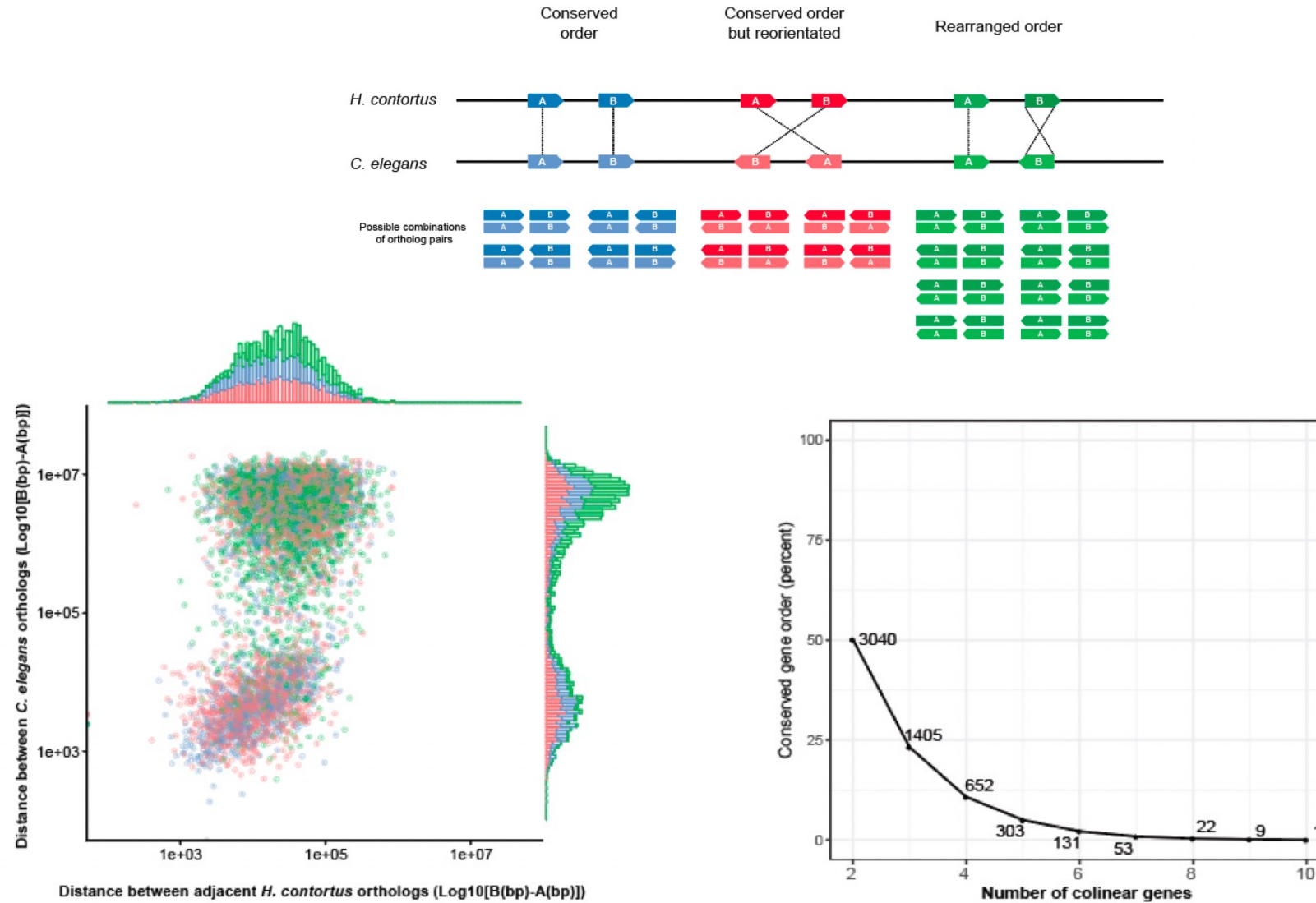


# Evolutionary insight using chromosome-scale genomes

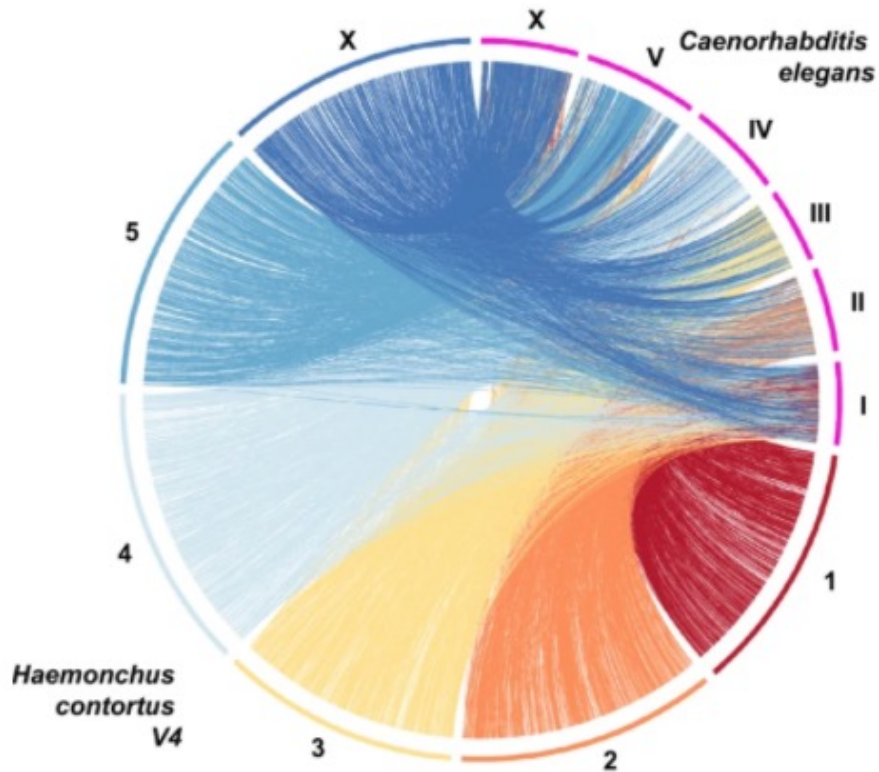




# Evolutionary insight using chromosome-scale genomes



# Shared parasite variation sheds light on adaption and migration

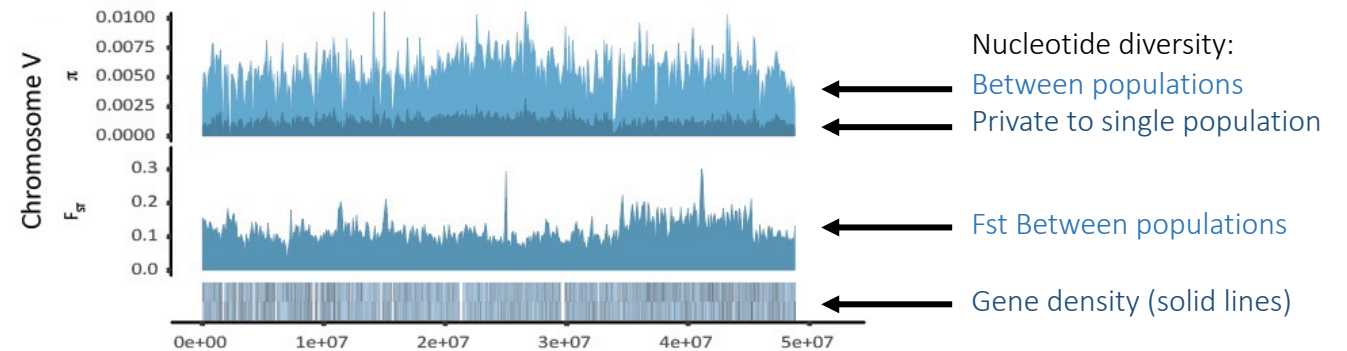


- Between species comparisons can tell us about deep evolutionary relationships
- Within species variation can inform more recent selection / adaptation
- How is genetic variation distributed among chromosomes?

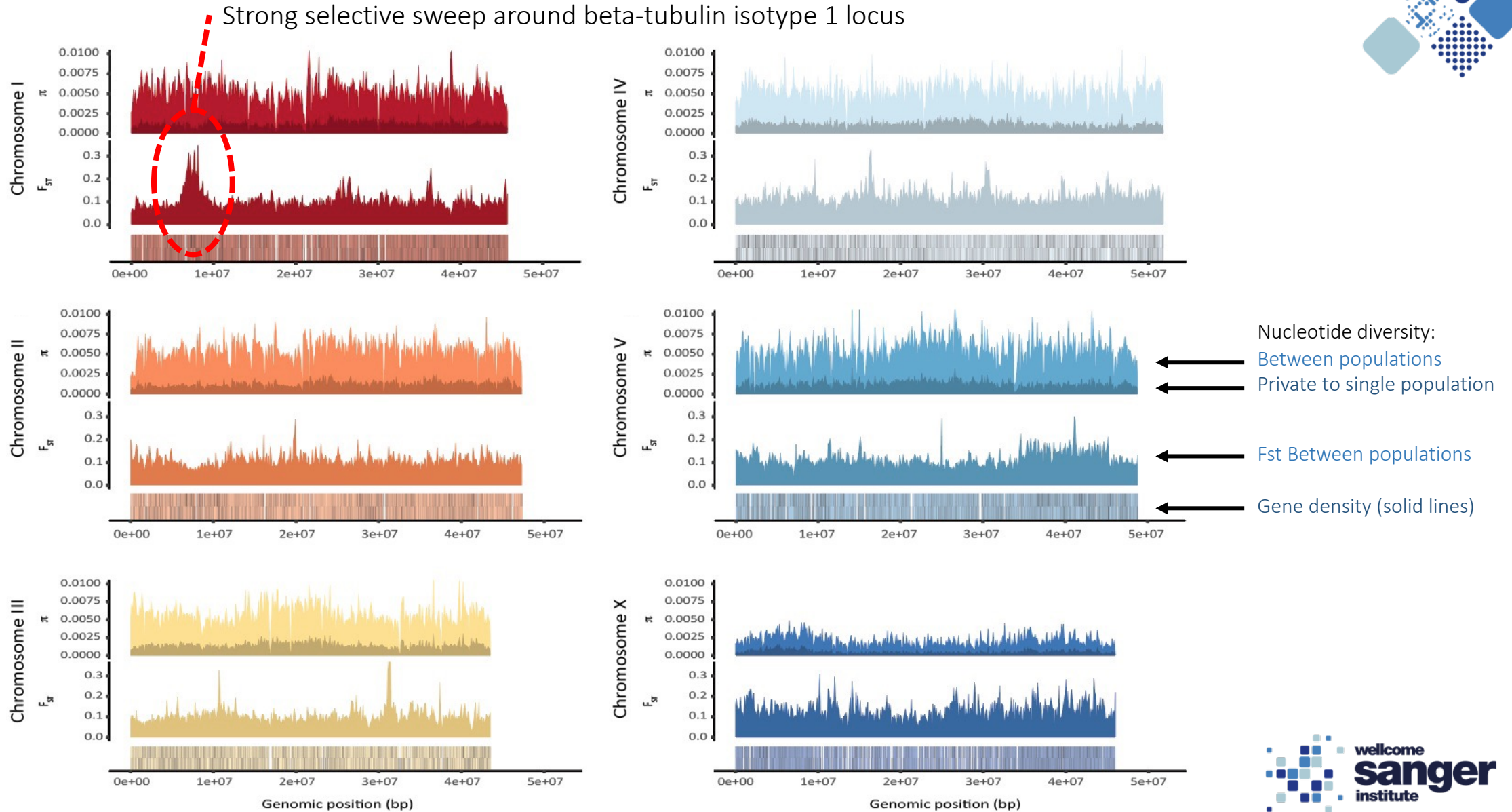
# Shared parasite variation sheds light on adaption and migration

Whole genome sequencing of *H. contortus*:

- 338 samples from 35 populations
- ~20 million single nucleotide variants



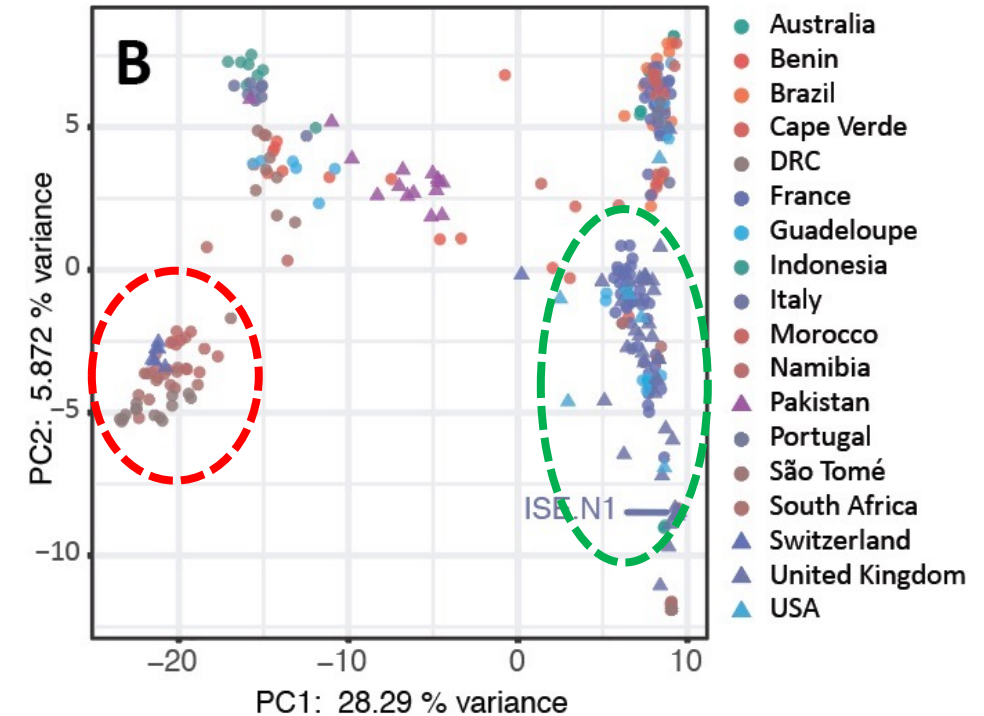
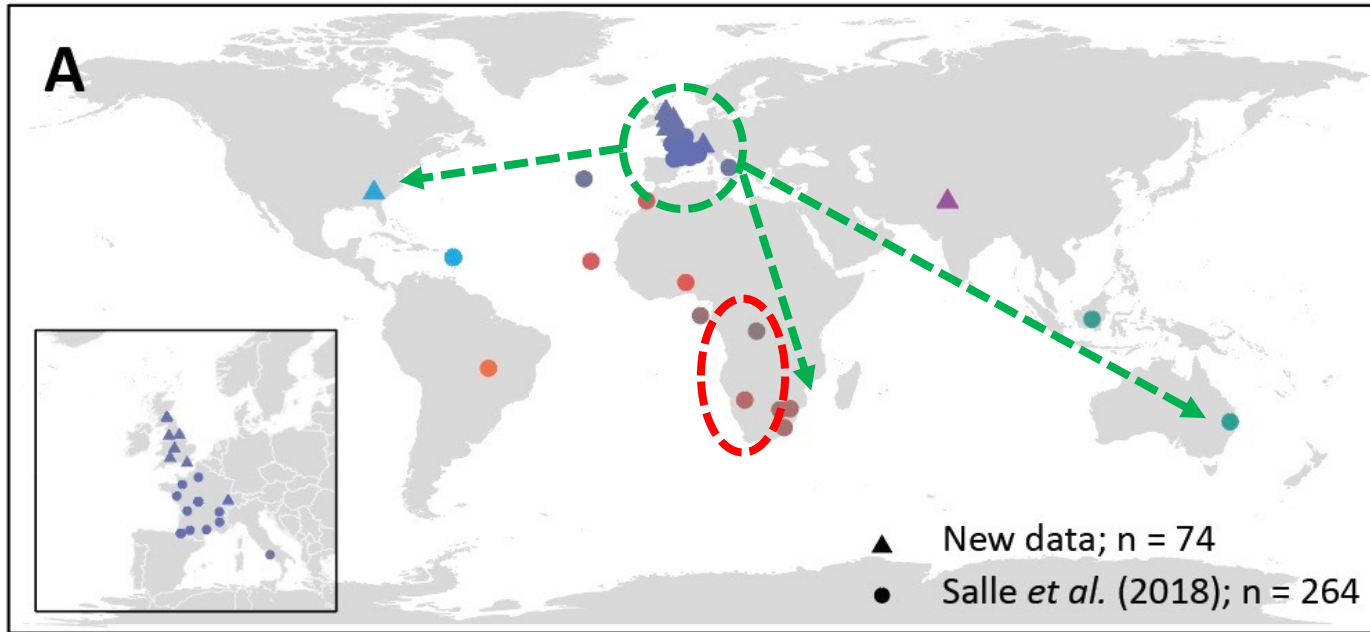
# Shared parasite variation sheds light on adaption and migration





# Shared parasite variation sheds light on adaption and migration

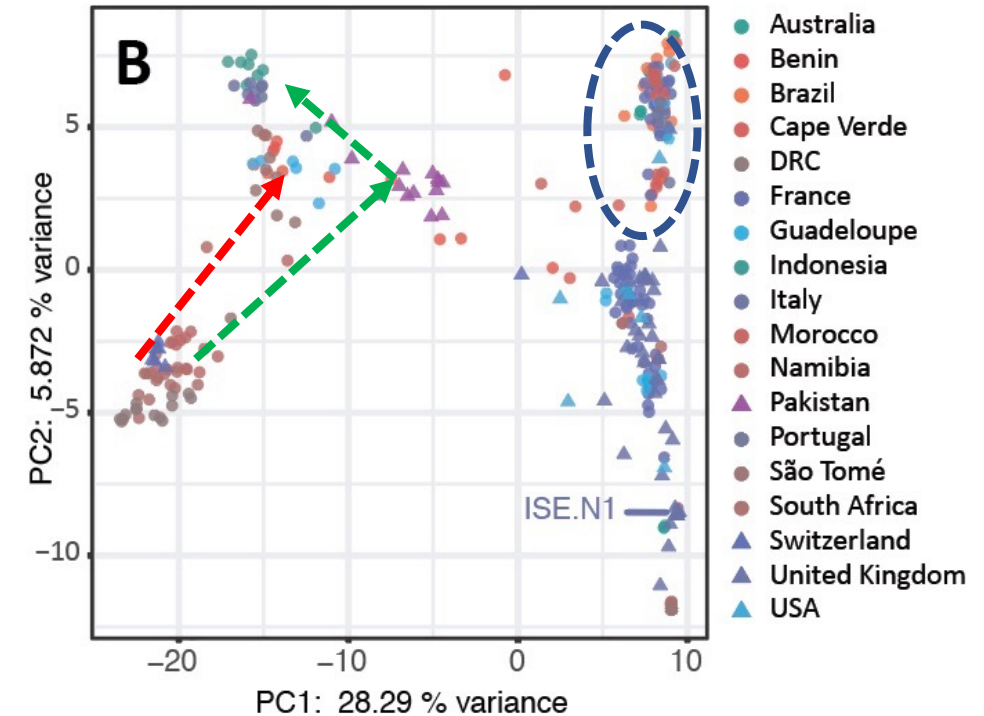
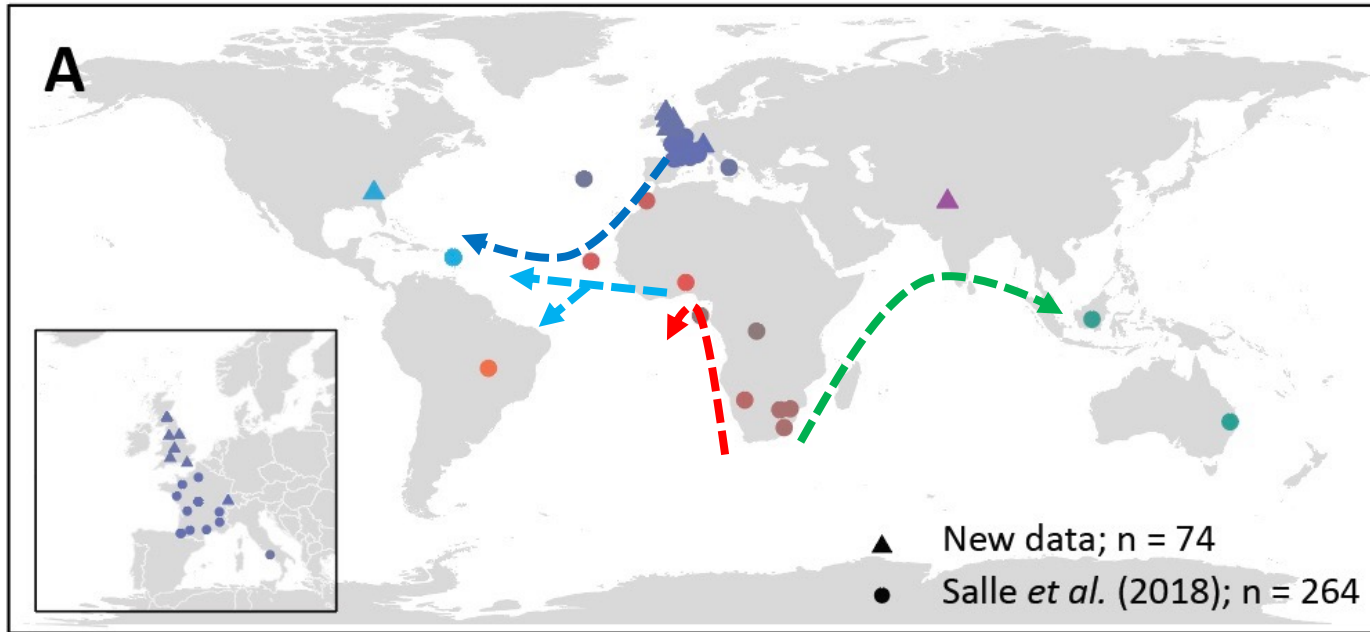
WGS: 338 samples from 35 populations



“Older” African diversity – South/Central

Modern European – spread broadly

# Shared parasite variation sheds light on adaption and migration



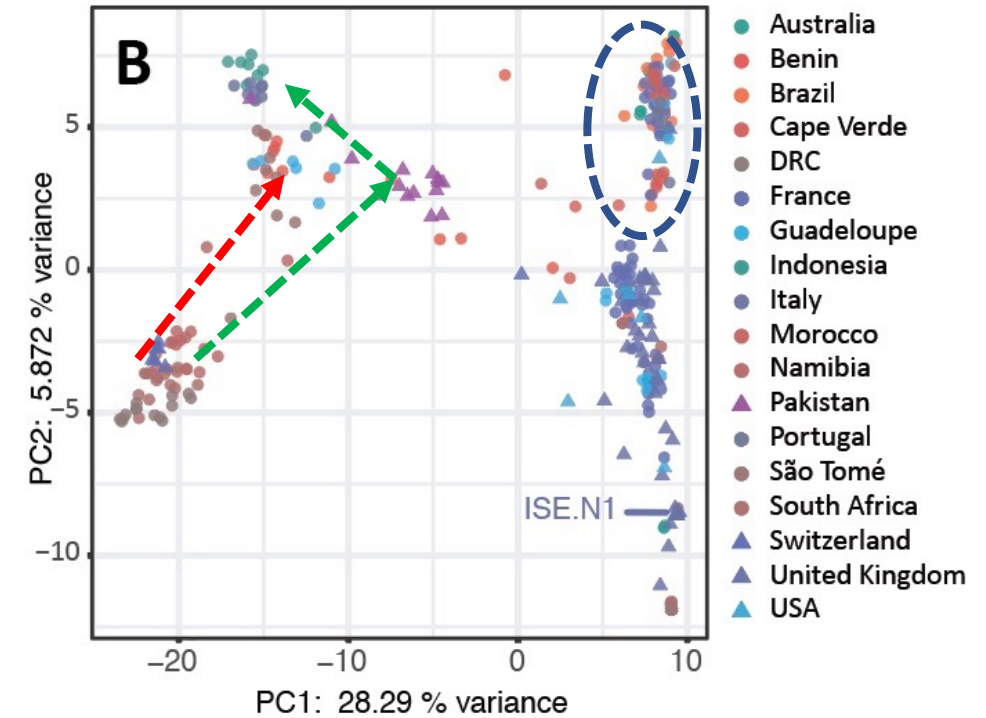
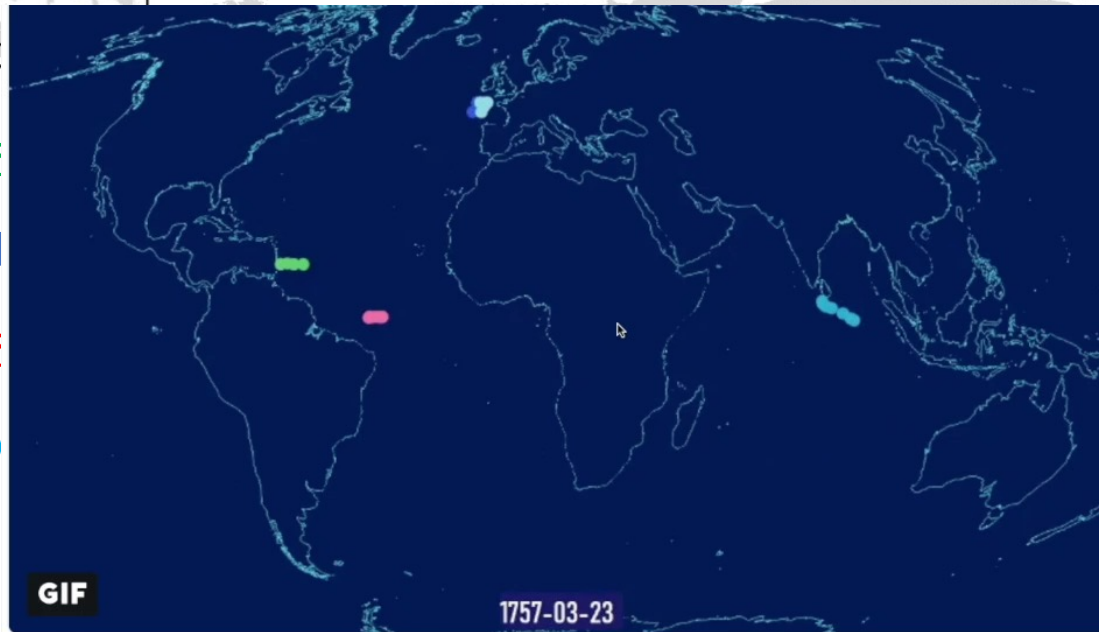
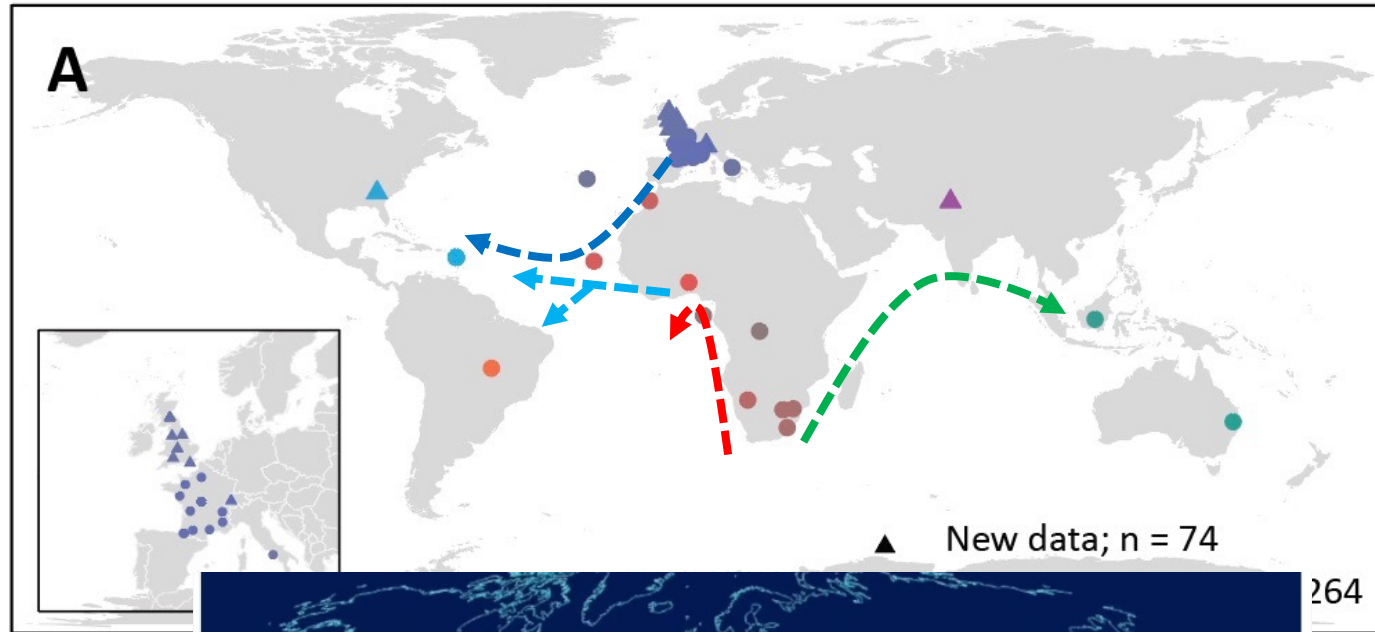
South Africa to Asia

Europe (France) to South America via Atlantic

South Africa toward Central / West Africa

West Africa to Americas

# Shared parasite variation sheds light on adaption and migration



# Comparative genomics of helminth parasites



- Provides great insight into helminth biology
  - what makes a worm?
  - What allows a worm to become an effective parasite?
- Helps describe deep evolutionary history
  - First genes, now chromosomes
  - Reconstructing divergence from last common ancestor
  - Understanding how/why chromosomes are structured
- Genetic variation allows us to explore recent evolutionary events
  - Transmission, migration, recrudescence
  - Adaptation under pressure - drugs, climate



# Acknowledgements



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Barbara Mable

Kirsty Maitland



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Umer Chaudry



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