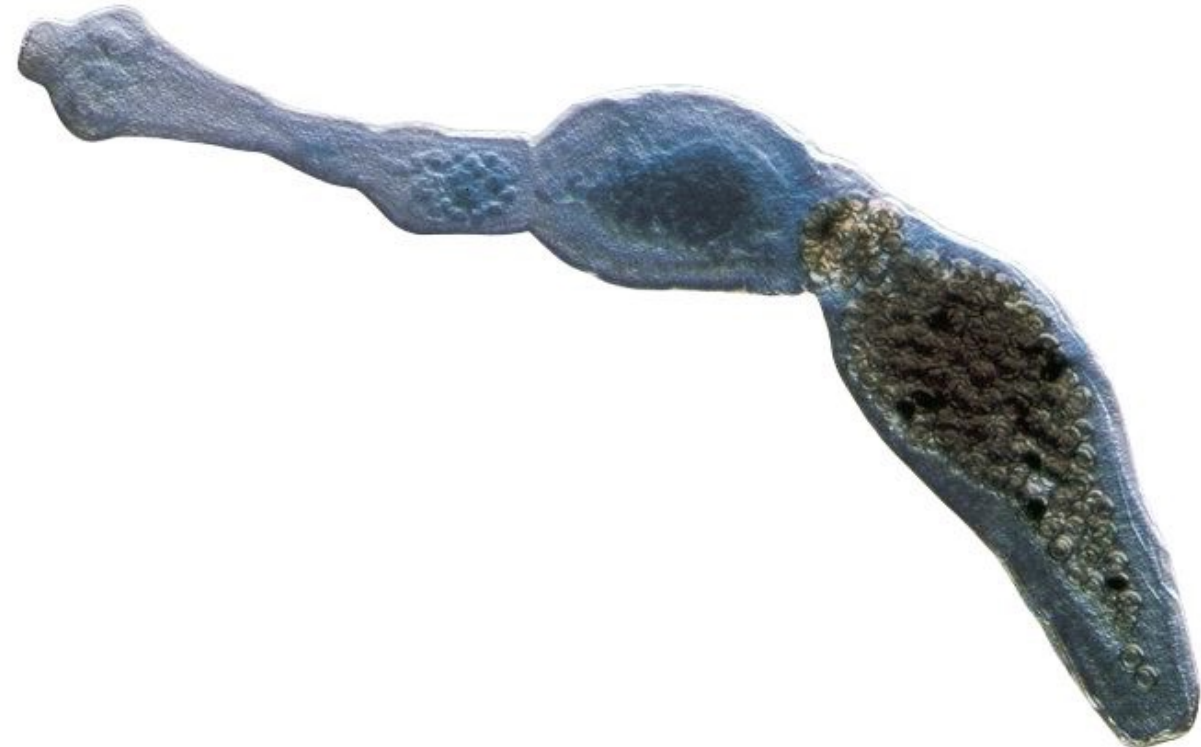# The analysis *of E.multilocularis* genome sequence

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 Intro. To Genomic "485"
Sunday 16/1/2022

outline

- Selected paper
- Organism:

  - Taxonomy
  - Physical charactstics
  - Parasitism
  - Geographic distribution
  - Life
  - Significance

- Sequenced sample info
- Sequencing strategy
- Sequencing method
- Genome assembly
- Interesting genome outcome

Genome paper

The genomes of four tapeworm species reveal adaptations to parasitism

Isheng J. Tsai[1,2]*, Magdalena Zarowiecki[1]*, Nancy Holroyd[1]*, Alejandro Garciarrubio[3]*, Alejandro Sanchez-Flores[1,3], Karen L. Brooks[1], Alan Tracey[1], Raúl J. Bobes[4], Gladis Fragoso[4], Edda Sciutto[4], Martin Aslett[1], Helen Beasley[1], Hayley M. Bennett[1], Jianping Cai[5], Federico Camicia[6], Richard Clark[1], Marcela Cucher[6], Nishadi De Silva[1], Tim A. Day[7], Peter Deplazes[8], Karel Estrada[3], Cecilia Fernández[9], Peter W. H. Holland[10], Junling Hou[5], Songnian Hu[11], Thomas Huckvale[1], Stacy S. Hung[12], Laura Kamenetzky[6], Jacqueline A. Keane[1], Ferenc Kiss[13], Uriel Koziol[13], Olivia Lambert[1], Kan Liu[11], Xuenong Luo[5], Yingfeng Luo[11], Natalia Macchiaroli[6], Sarah Nichol[1], Jordi Paps[10], John Parkinson[12], Natasha Pouchkina-Stantcheva[14], Nick Riddiford[14,15], Mara Rosenzvit[6], Gustavo Salinas[9], James D. Wasmuth[16], Mostafa Zamanian[17], Yadong Zheng[5], The *Taenia solium* Genome Consortium†, Xuepeng Cai[5], Xavier Soberón[3,18], Peter D. Olson[14], Juan P. Laclette[4], Klaus Brehm[13] & Matthew Berriman[1]

Tapeworms (Cestoda) cause neglected diseases that can be fatal and are difficult to treat, owing to inefficient drugs. Here we present an analysis of tapeworm genome sequences using the human-infective species *Echinococcus multilocularis*, *E. granulosus*, *Taenia solium* and the laboratory model *Hymenolepis microstoma* as examples. The 115- to 141-megabase genomes offer insights into the evolution of parasitism. Synteny is maintained with distantly related blood flukes but we find extreme losses of genes and pathways that are ubiquitous in other animals, including 34 homeobox families and several determinants of stem cell fate. Tapeworms have specialized detoxification pathways, metabolism that is finely tuned to rely on nutrients scavenged from their hosts, and species-specific expansions of non-canonical heat shock proteins and families of known antigens. We identify new potential drug targets, including some on which existing pharmaceuticals may act. The genomes provide a rich resource to underpin the development of urgently needed treatments and control.

- My organism: Taxonomy

  ➢ SK: Eukaryote

  ➢ K: metazoan

  ➢ P:Platyhelminthes

  ➢ C:cestode

  ➢ O: cyclophyllidea

 ➢ F:Taeniidae

  ➢ G: Echinococcus

  ➢ S: multilocularis

Physical characteristics

❖ *E.maltilucolaris* cause hydatid disease that cause by the
proliferation of larval tapeworms in vital organ.

❖ Are among the most severe parasitic disease in humans.

❖ Laval tapeworms can persist asymptomatically in human host of
decades.
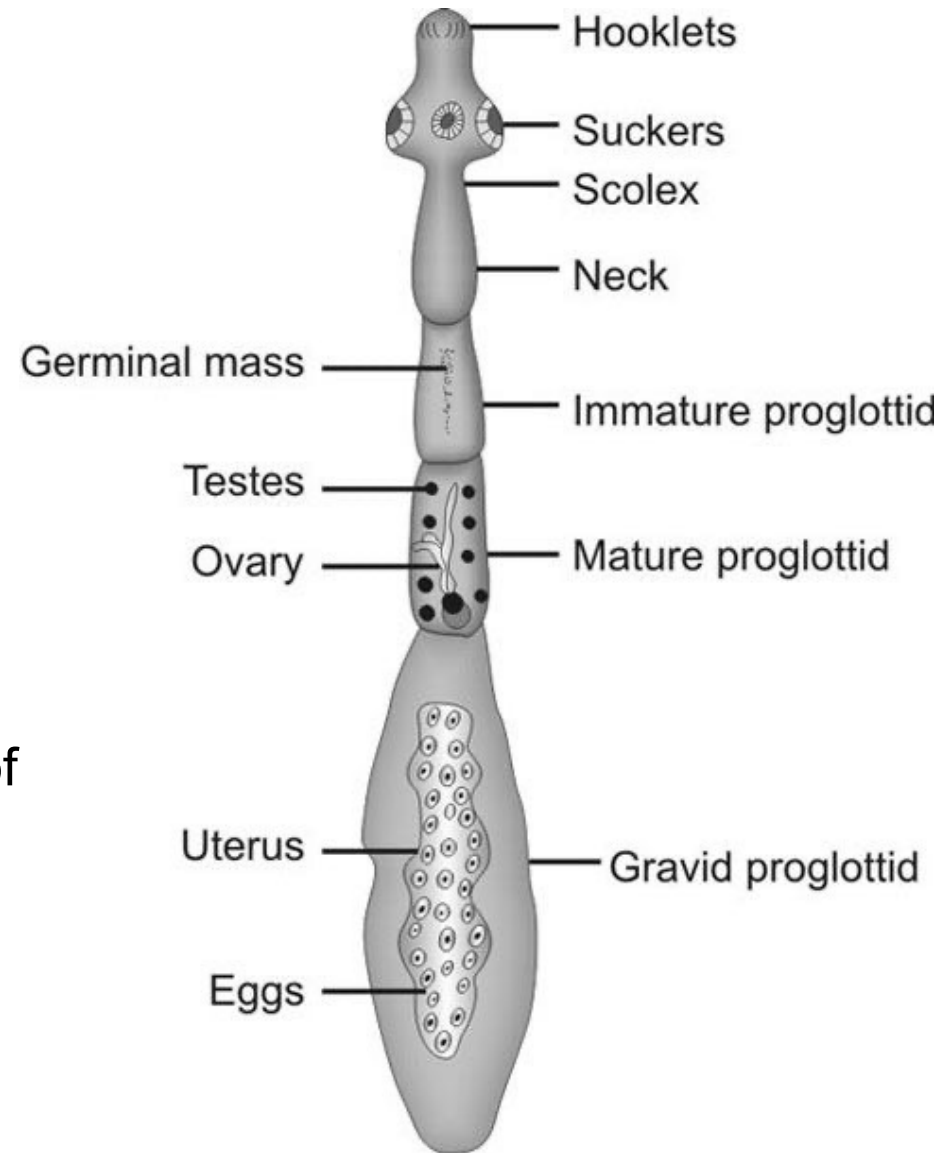
Parasitism

❖ Can passively transmitted between hosts and parasitize virtually every vertebrate species.

❖ Their morphological adaptations to parasitism include:

• The absence of a gut, head and light sensing organ.

• They passes a unique surface that is able to withstand host - stomach acid and bile but is still penetrable enough to absorb nutrients.
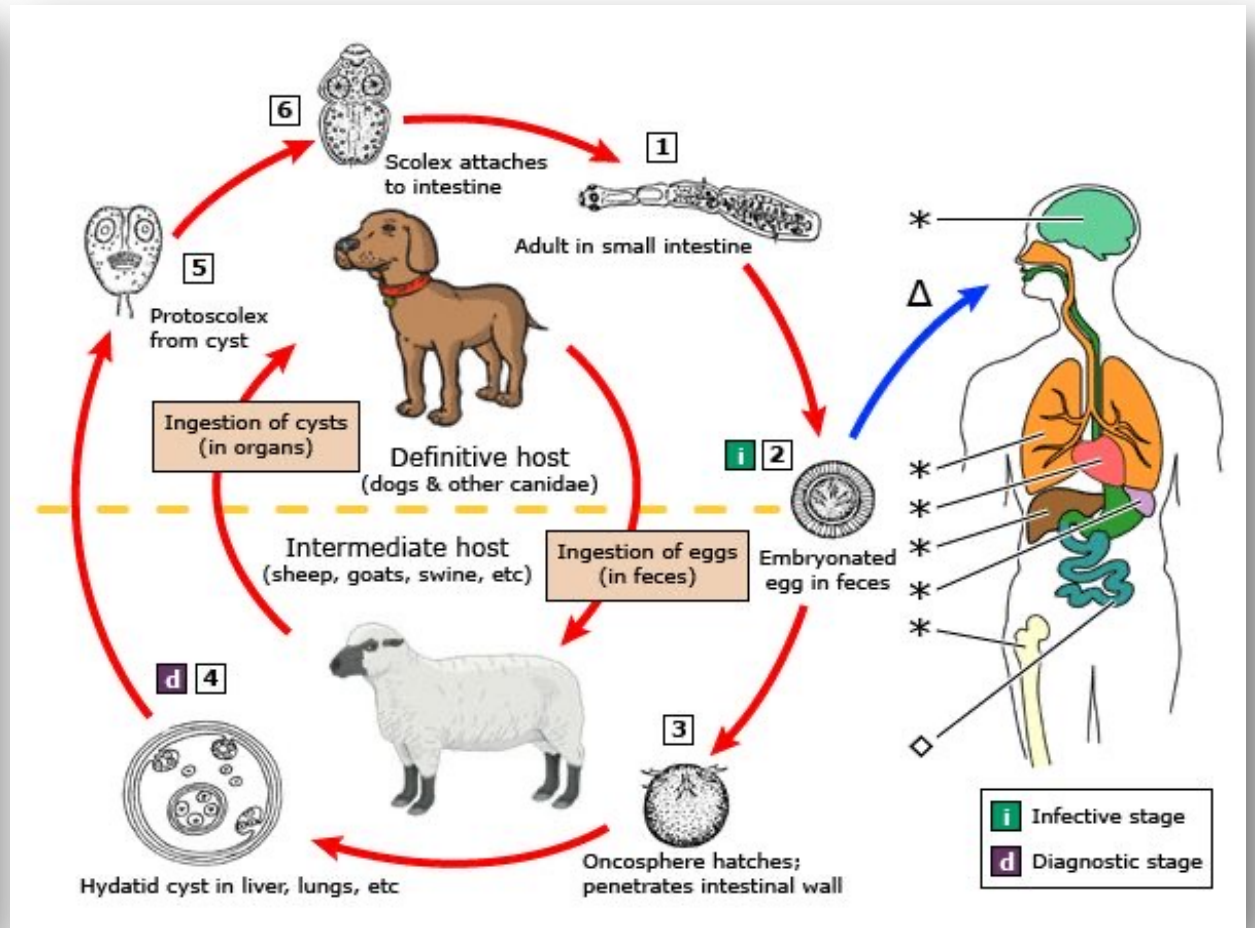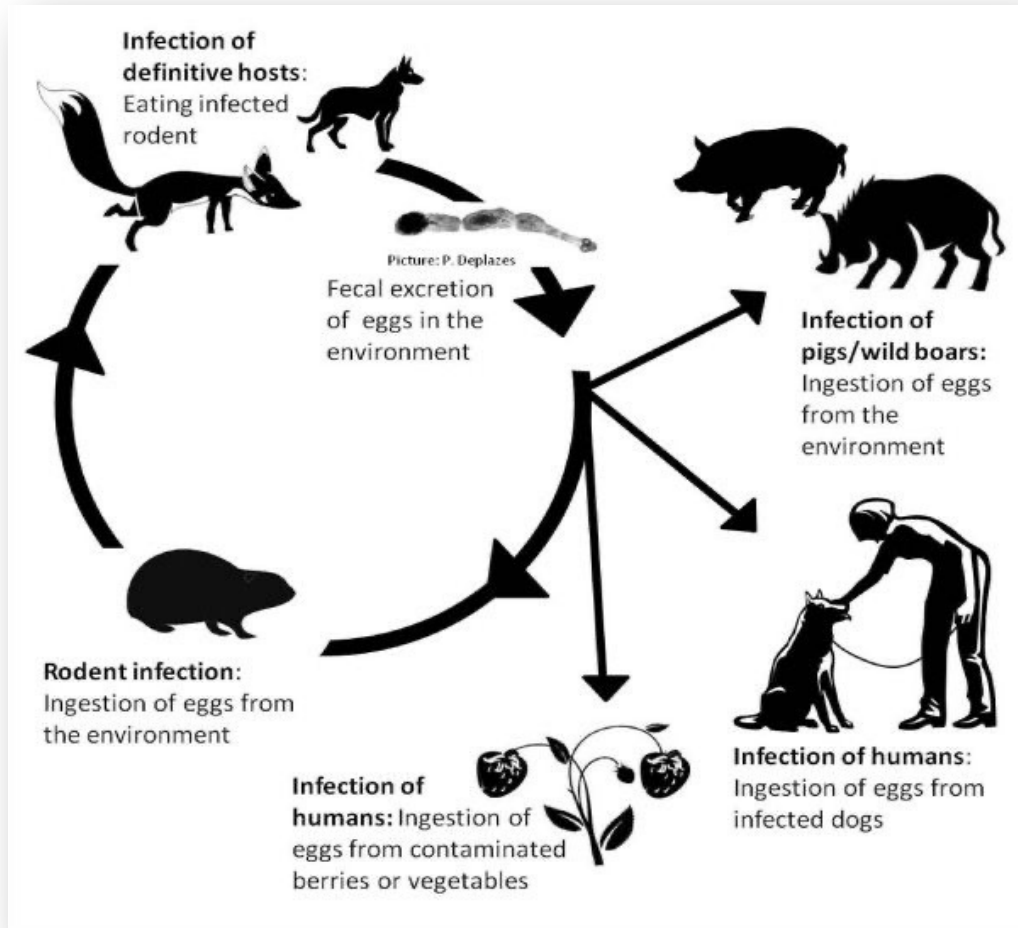

Echinococcus mulitilocularis
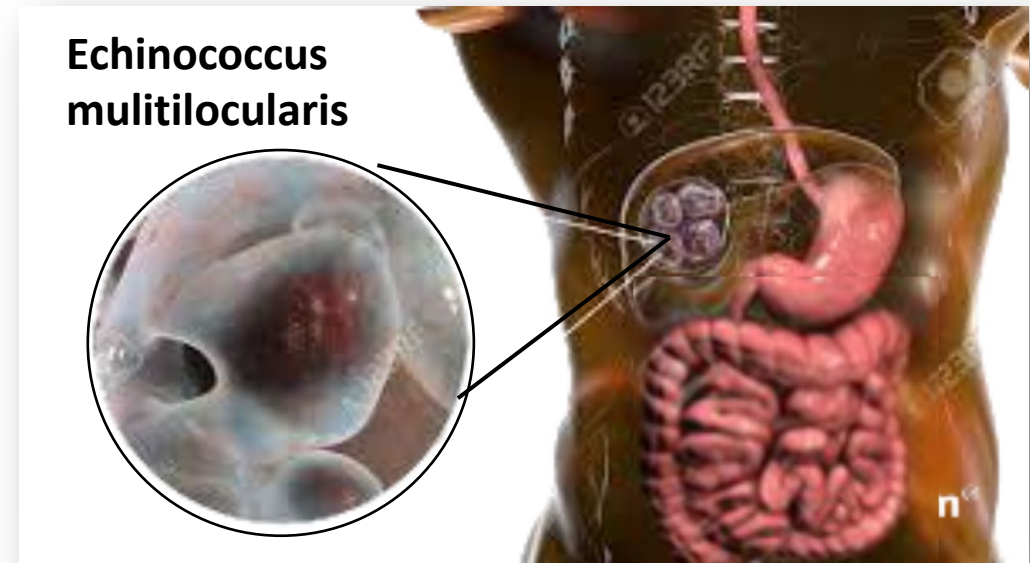
Geographic distribution

➤ Tapeworm infections are highly prevalent world wide.
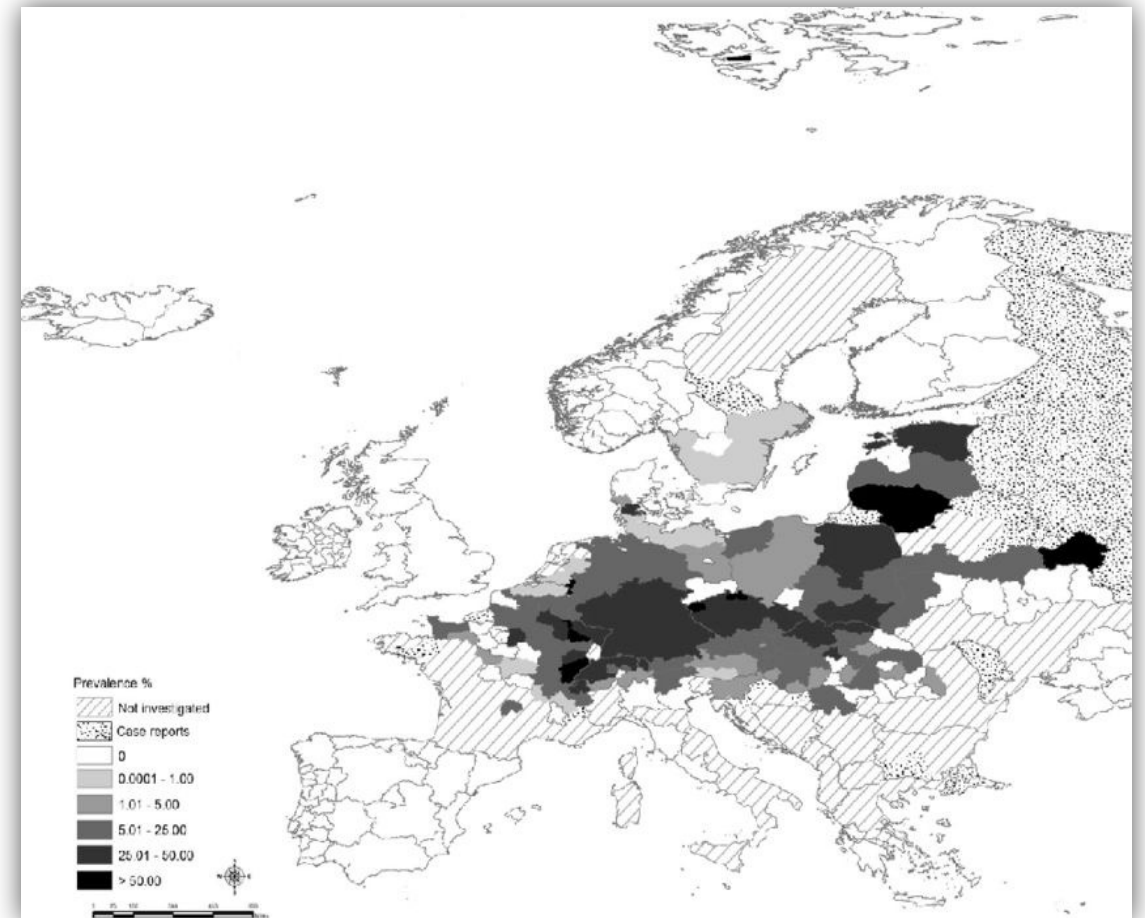
Life cycle

Significance

❖ present a high- quality of human infective reference tapeworm genome of a human infective fox tapeworm (Echinococcus multilocularis) also present the genomes of three other species, for comparison E. granulous, Taenia solium, Hymenolepis microstoma.

❖ They have mined the genomes to provide starting point for developing urgently needed therapeutic measure against tapeworm.

❖ access to the complete genomes of several tapeworms will accelerate the pace at which new took and treatments to combat tapeworm infection can be discovered.
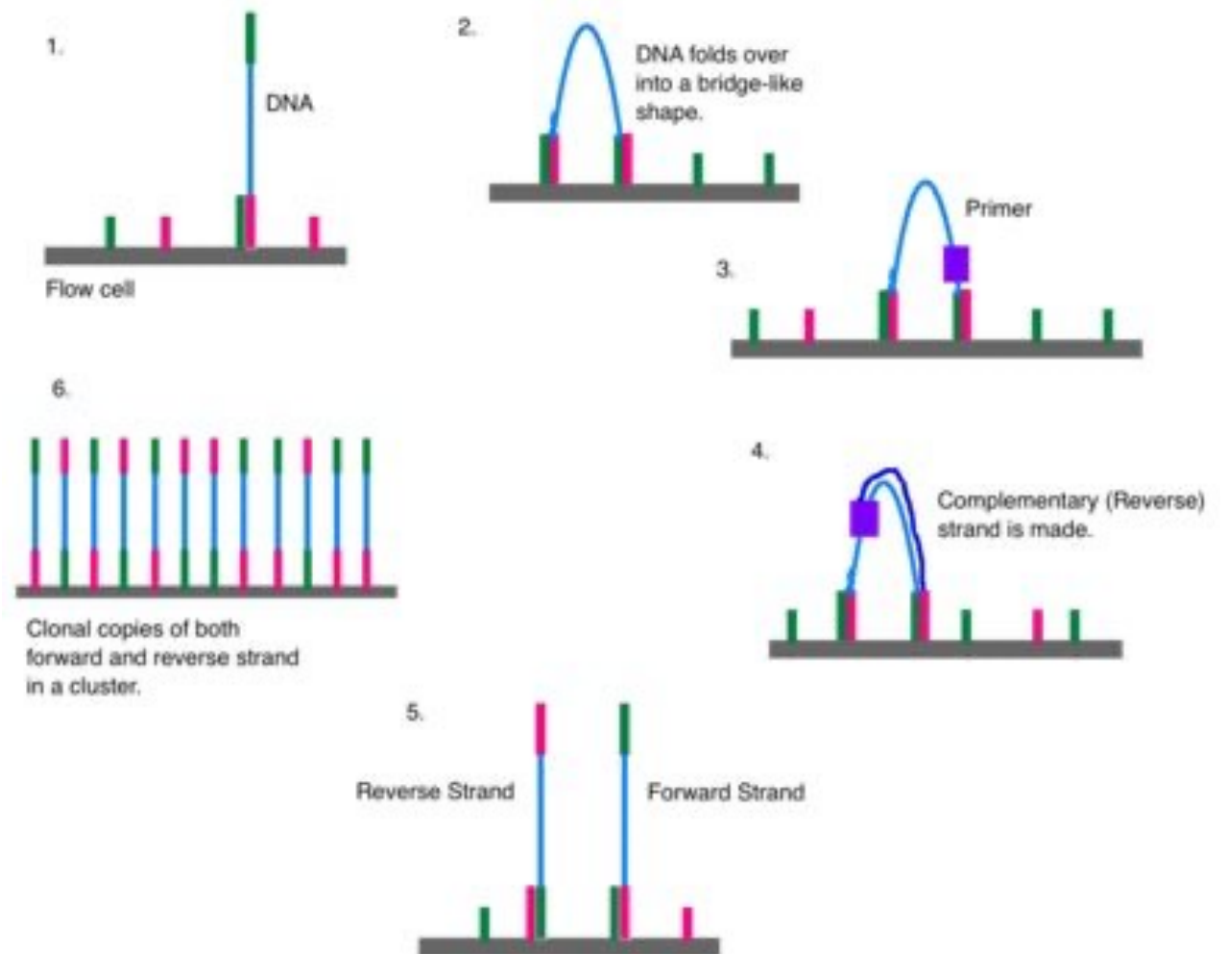
Sequence sample information

➢ The E. multilocularis reference genome was sequenced from the isolate JAVA05, isolate from the live of naturally infected crab-eating macaque.
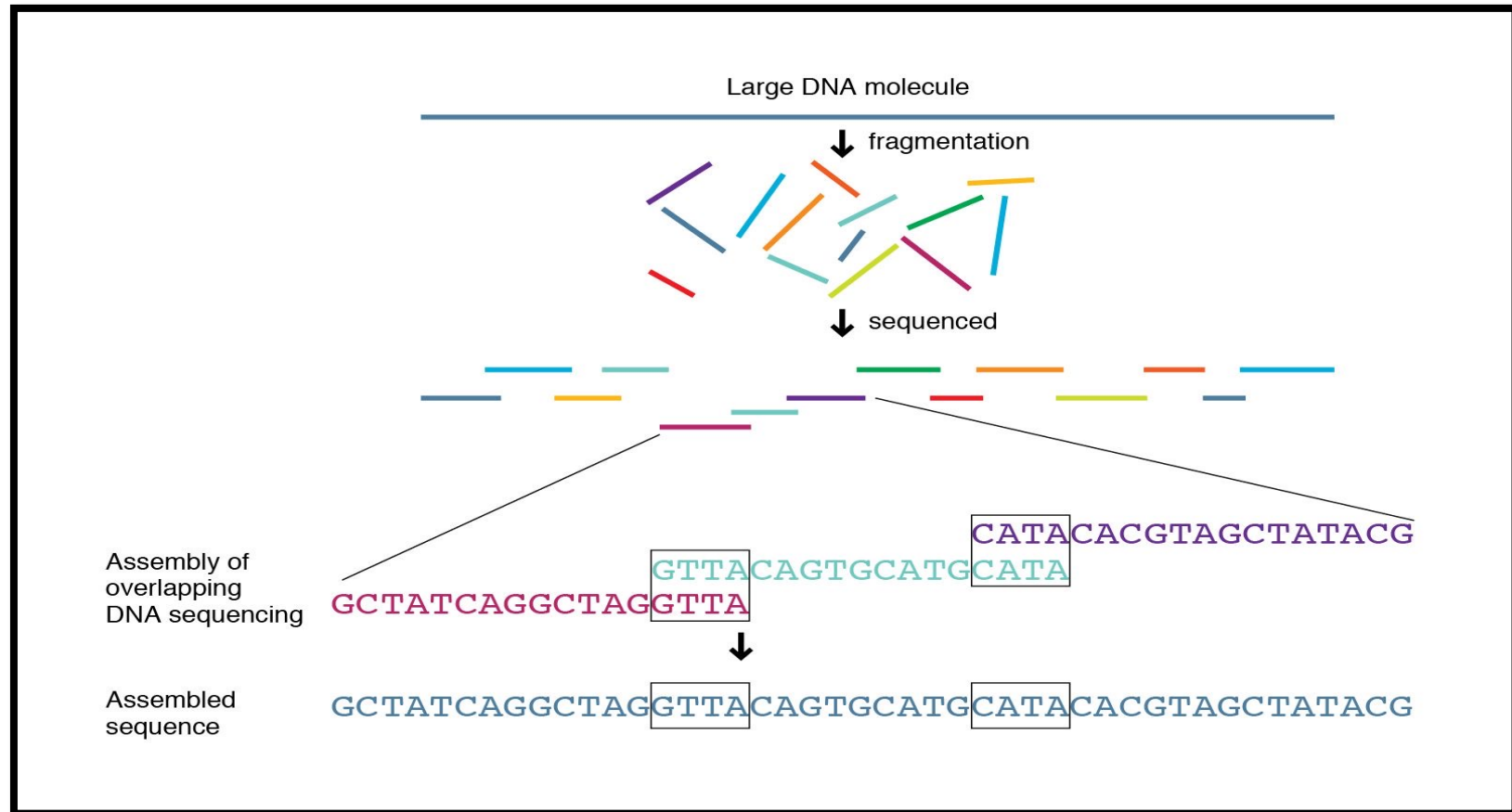
Sequence method

➢ Illumina sequence method.

Sequence strategy

➢ Whole genome shotgun

Genome assembly

➢ Genome coverage = 80 X

➢ Genome size = 115 Mb

➢ N50 = 13.8 Mb

➢ Largest scaffold = 20.1 Mb

	Genome Size (Mb)	genes	repeat content (%)	N50 (Mb)	nN50	Largest scaffold (Mb)	N90 (kb)	nN90
E. multilocularisa	115	10345	10.9	13.8	4	20.1	2900	10
E. granulosusb	114.9	10231	7.6	5.2	6	16	200	42
T. solium	122.3	12490	9.9	0.07	439	0.7	5	2878
H. microstoma	141.1	10241	10.2	0.5	75	2.4	82	304
S. mansonic	364.5	10852	58.7	32.1	4	65.5	547	68

Interesting Genome Outcome

- Specialized metabolism

❑ Tapeworms have specialized detoxification pathways, and a metabolism that finely tuned to depend on nutrients from their hosts.

- Stem cell specializations

❑ Tapeworms lack a specific gene for stem cells ubiquitously.

- Novel Drug targets

❑ Albendazole, Mebendazole, and niclosamide.

Questions

❖ What is the sequencing method was used? And why?

❖ How many tapeworm's species in my paper?