

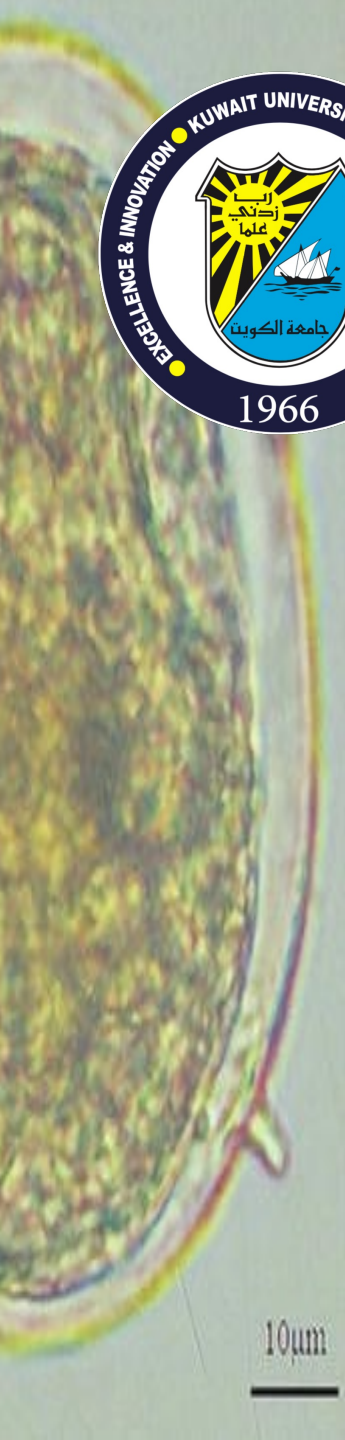


A look into the genome of *S.japanicom* (blood fluke)

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Intro. to genomics (485)

1/16/2022



Outline

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ARTICLES

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

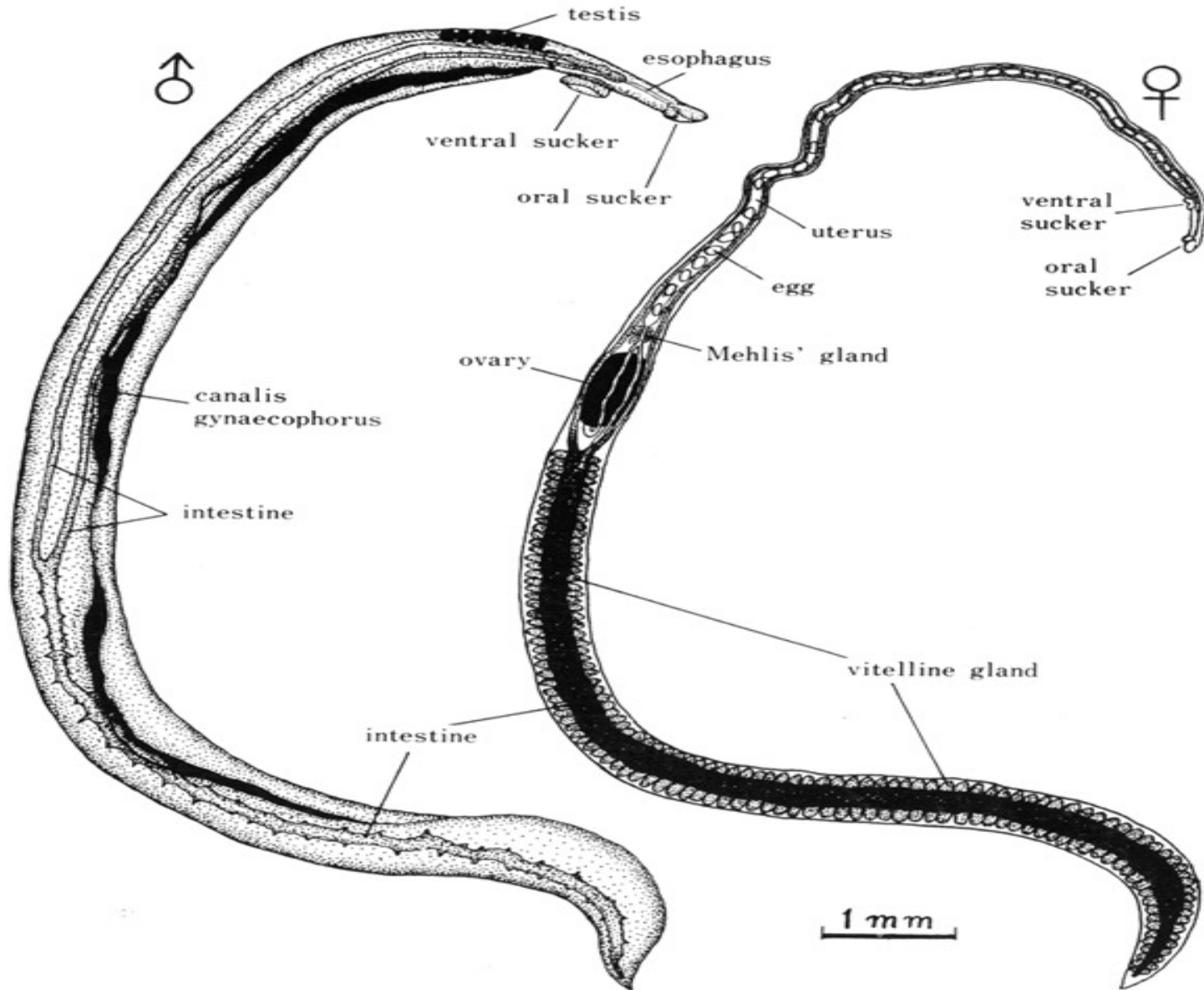
The *Schistosoma japonicum* Genome Sequencing and Functional Analysis Consortium*

Schistosoma japonicum is a parasitic flatworm 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 global insight into the molecular architecture and host interaction of this complex metazoan pathogen, revealing that it 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.

My organism: Taxonomy

- SK: Eukaryota
 - K: Metazoa
 - P: Platyhelminthes
 - C: Trematoda
 - O: Strigeidida
 - F: Schistosomatidae
 - ***G: Schistosoma***
 - ***S: japonicum***

My organism: Physical characteristic



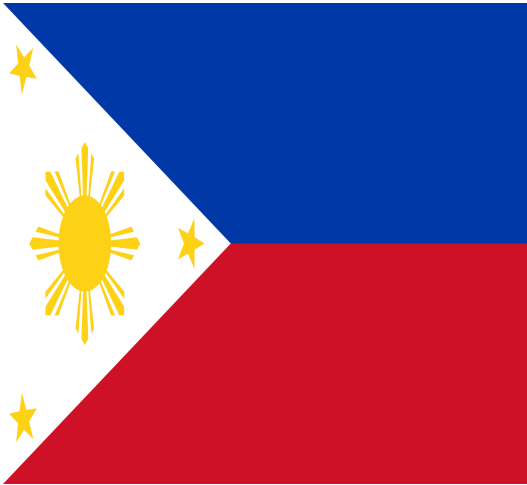
My organism: Parasitism

- It is a parasitic flatworm that cause human schistosomiasis, a significant cause of morbidity in China and the Philippines. And considered a major risk for 66 million people living in southern China.

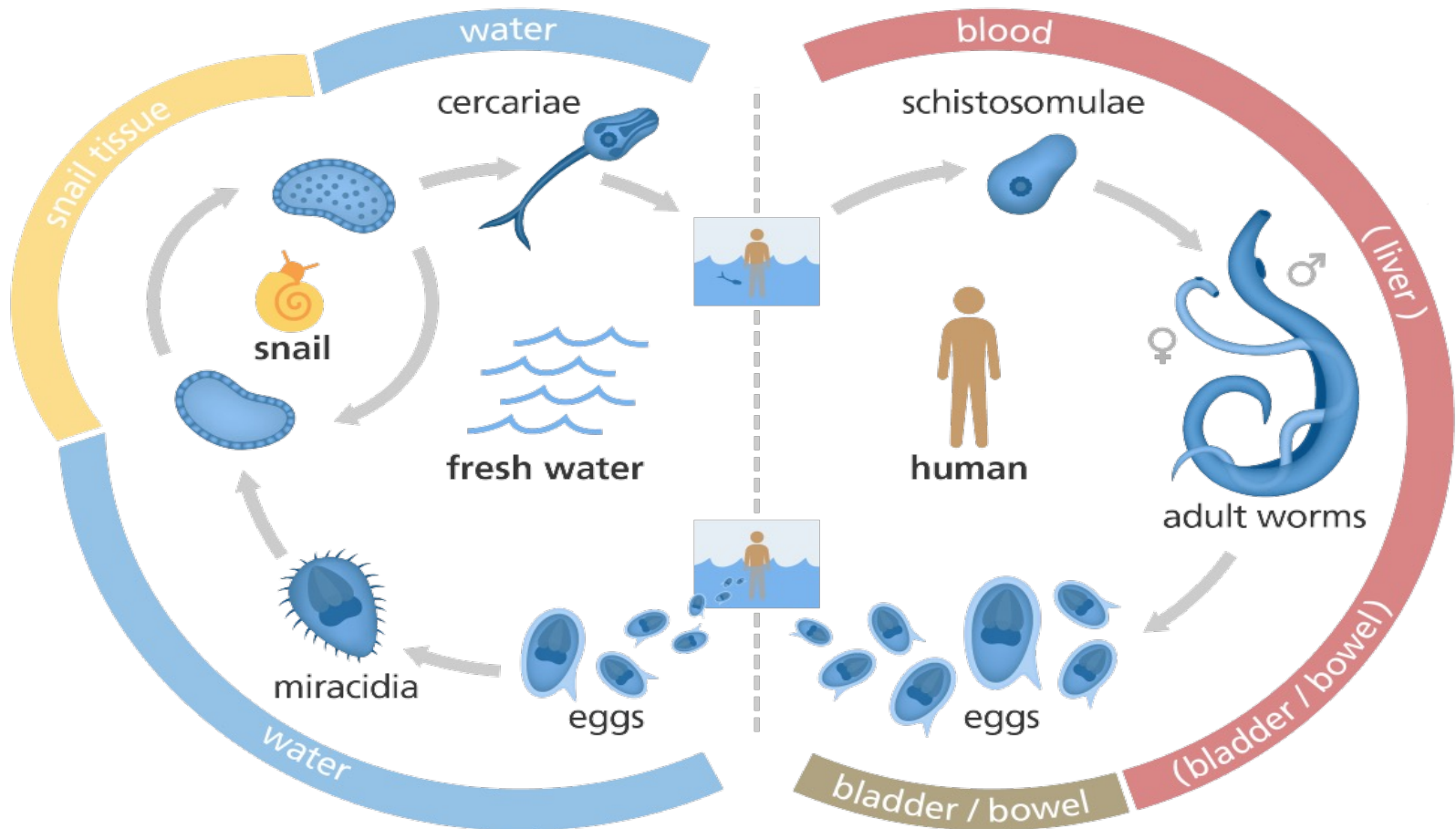


My organism: Geographic distribution

- Prevalent in the Philippines, parts of Indonesia, and southern China.



My organism: Life cycle



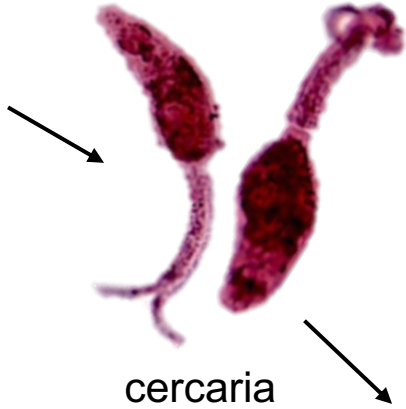
My organism: Significance

- The *S.japonicum* genome was sequenced to aid in the development a new contributions for schistosomiasis control.

Sequence sample info



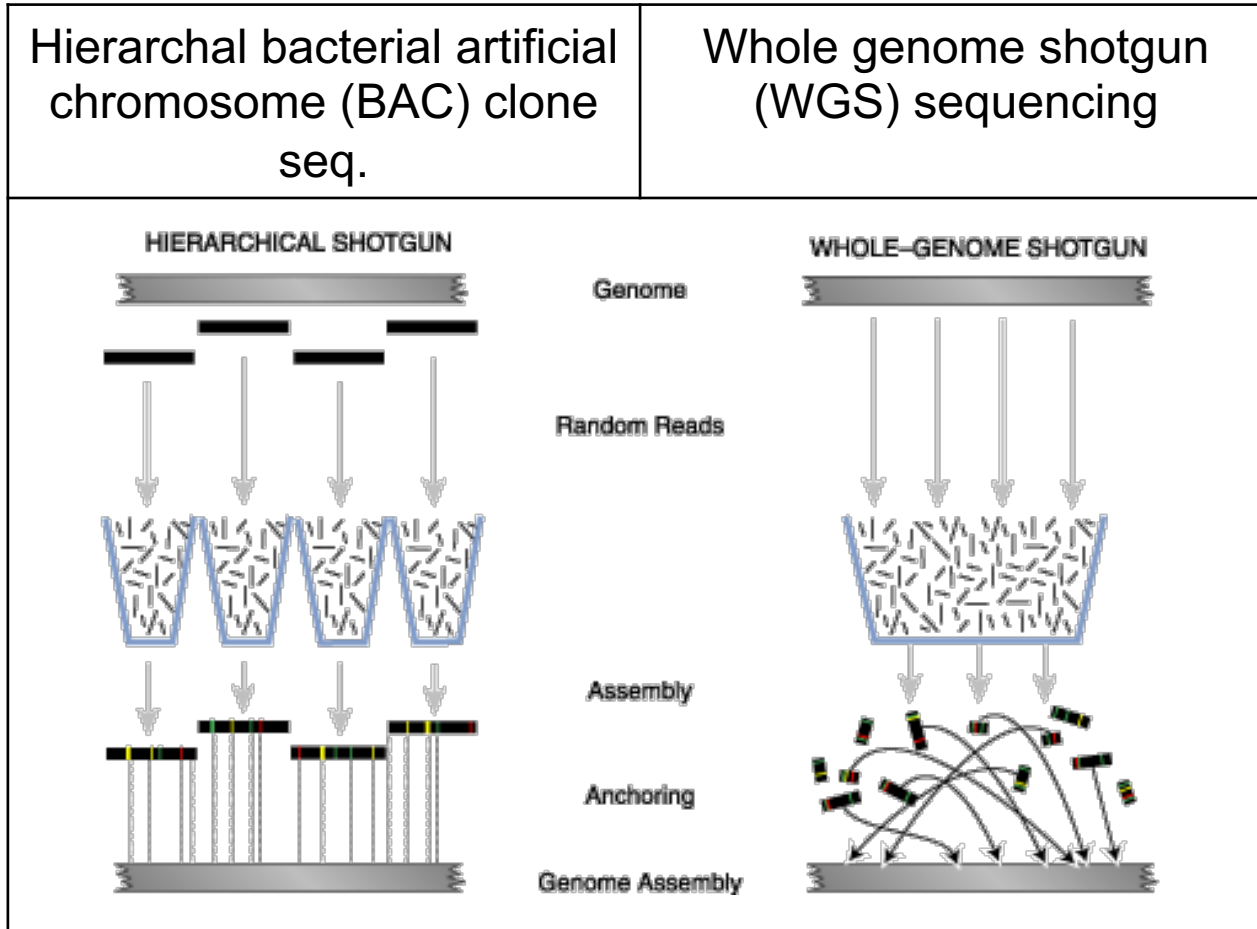
Snail



cercaria

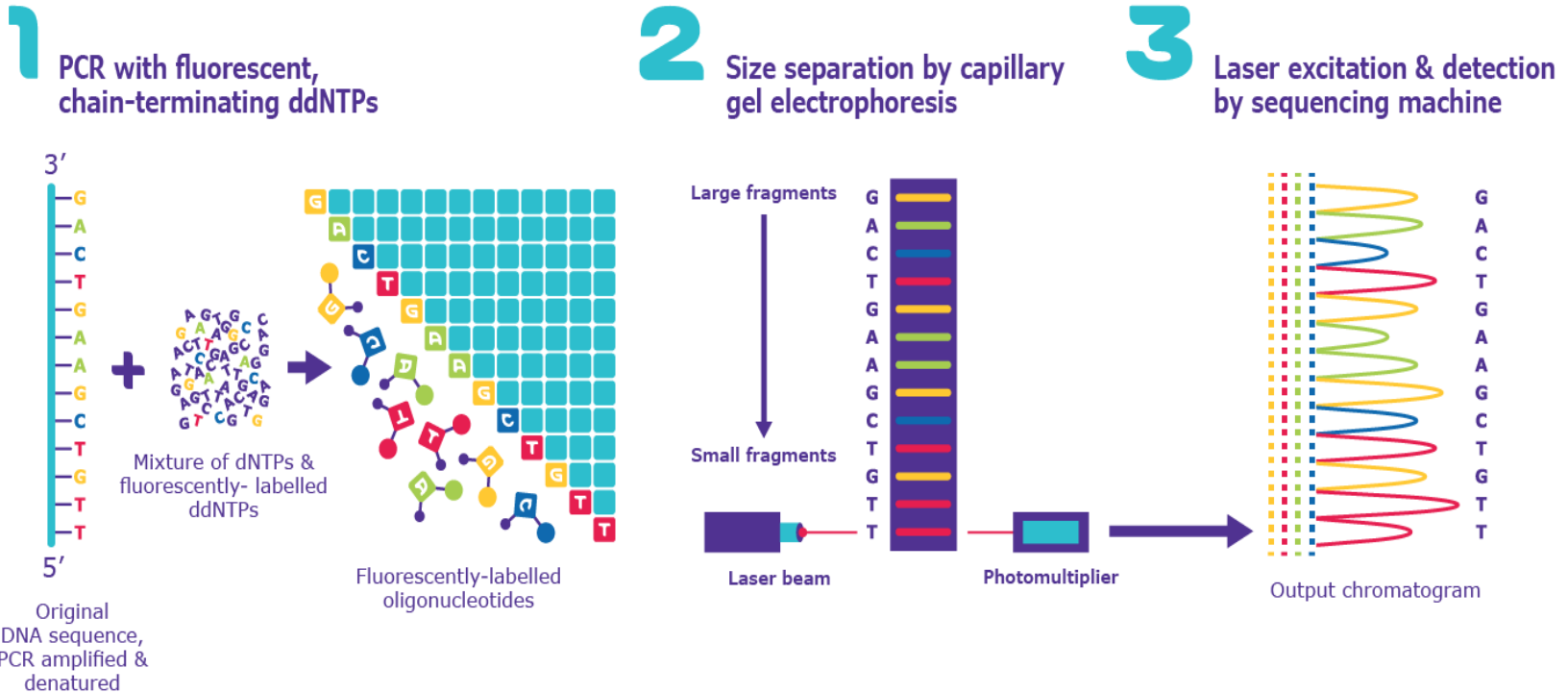


Sequencing strategy



Sequencing method

- Capillary DNA sequence (Sanger) :



Genome assembly

- Modified PHUSION package for WGS reads, then BLASTN was used to relocate the read to the contig consensus.

Assembled scaffolds	397 Mb
Protein coding gene	13 469
Single nucleotide polymorphism	557 739
Coverage	5.87X
N50	6 Kb
N50 contig	17 Kb
LTRs	6.16 %
Non- LTR	12.63 %
SINEs	1.84%

Interesting genome outcome

- A total of 657 repeat families/elements and they were constituting 159 MB (40.1%). Among them:
 - 29 retrotransposons were found (18 LTR, 4 non-LTR, 3 *Penelope* like element)
- It was fascinating to observe that schistosomes share more orthologues with the vertebrates such as *H. sapiens* (4,324 pairs).
- 1000 protein dominant have been abandoned by *S.japonicum* the loss of these dominant partly could lead for the adaptation of a parasitic way of existence.
- The finding of expanded gene families of schistosomes would help if finding clues to need of parasitic lifestyle.

Questions:

- What is *S.japonicum* common name ?
- What is unique about retrotransposons genes?

Hope you enjoyed the brief look to the
S.japonicum.



Thank you