The Genome of Ascaris suum

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Introduction to Genomics 485

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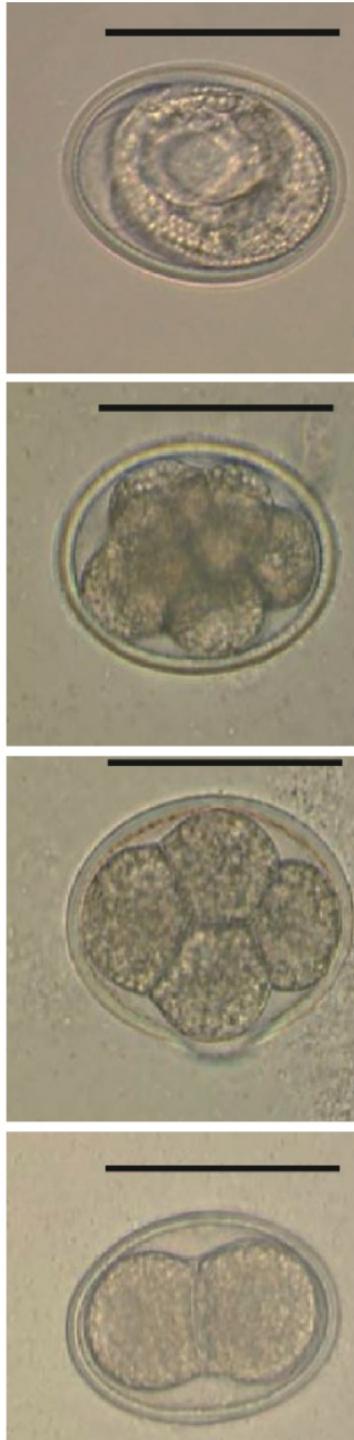

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Selected paper

LETTER

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Ascaris suum draft genome

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Parasitic diseases have a devastating, long-term impact on human health, welfare and food production worldwide. More than two billion people are infected with geohelminths, including the roundworms *Ascaris* (common roundworm), *Necator* and *Ancylostoma* (hookworms), and *Trichuris* (whipworm), mainly in developing or impoverished nations of Asia, Africa and Latin America[1]. In humans, the diseases caused by these parasites result in about 135,000 deaths annually, with a global burden comparable with that of malaria or tuberculosis in disability-adjusted life years[1]. *Ascaris* alone infects around 1.2 billion people and, in children, causes nutritional deficiency, impaired physical and cognitive development and, in severe cases, death[2]. *Ascaris* also causes major production losses in pigs owing to reduced growth, failure to thrive and mortality[2]. The *Ascaris*–swine model makes it possible to study the parasite, its relationship with the host, and ascariasis at the molecular level. To enable such molecular studies, we report the 273 megabase draft genome of *Ascaris suum* and compare it with other nematode genomes. This genome has low repeat content (4.4%) and encodes about 18,500 protein-coding genes. Notably, the *A. suum* secretome (about 750 molecules) is rich in peptidases linked to the penetration and degradation of host tissues, and an assemblage of molecules likely to modulate or evade host immune responses. This genome provides a comprehensive resource to the scientific community and underpins the development of new and urgently needed interventions (drugs, vaccines and diagnostic tests) against ascariasis and other nematodiases.

>2 kb) (Table 1) with a mean GC-content of 37.9%. This genome has few repetitive sequences (about 4.4% of the total assembly) relative to that reported for other metazoan genomes sequenced to date[3–6], probably as a result of chromatin diminution[7]. We identified 424 distinct retrotransposon sequences (see Supplementary Tables 1–3) representing at least 22 families (8 long terminal repeats (LTRs), 12 long interspersed elements (LINEs) and 2 short interspersed elements (SINEs)), with *Gypsy*, *Pao* and *Copia* classes predominating for LTRs ($n = 97$, 85 and 60, respectively) and CR1, L1, and reverse transcriptase encoding RTE-RTE classes predominating for non-LTRs ($n = 29$, 28 and 21, respectively). We also identified eight families of DNA transposons (91 distinct sequences in total), of which *MuDr*, *En-Spm* and *Merlin* ($n = 12$, 9 and 8, respectively) predominated. We predicted 18,542 genes (14,783 supported by transcriptomic data), with a mean total length of 6.5 kb, exon length of 153 bp and a mean of 6.4 exons per gene (see Supplementary Fig. 2). Compared with the nematodes (roundworms) *Caenorhabditis elegans*[3], *Pristionchus pacificus*[8], *Brugia malayi*[9] or *Meloidogyne hapla*[10], overall, the *A. suum* genes are significantly longer (see Supplementary Table 2), relating primarily to expansions of intronic regions (mean 1.1 kb).

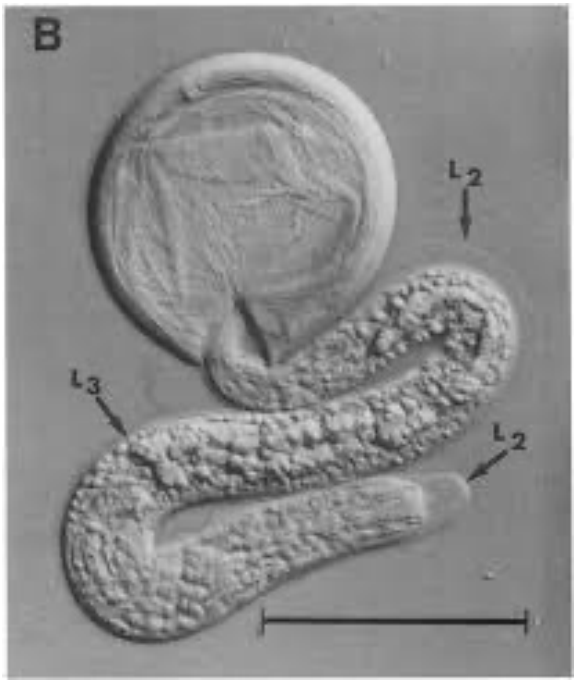
Most (78.2%) of the predicted *A. suum* genes (Fig. 1) have a homologue (BLASTp cut-off $\leq 10^{-5}$) either in *C. elegans* ($n = 12{,}779$; 68.9%), *B. malayi* (12,853; 69.3%), *M. hapla* (10,482; 56.5%) or *P. pacificus* (11,865; 64.0%), with 8,967 being homologous among all species examined, and 4,042 (21.8%) being 'unique' to *A. suum* (see Fig. 1). Of the genes with homology to *C. elegans* or *B. malayi*, ~50%

Organism: Taxonomy

- Super Kingdom: Eukaryota
  - Kingdom: Metazoa
    - Phylum: Nematoda
      - Class: Chromadorea
        - Order: Rhabditida
          - Family: Ascarididae
            - **Genus: Ascaris**
            - **Species: Suum**

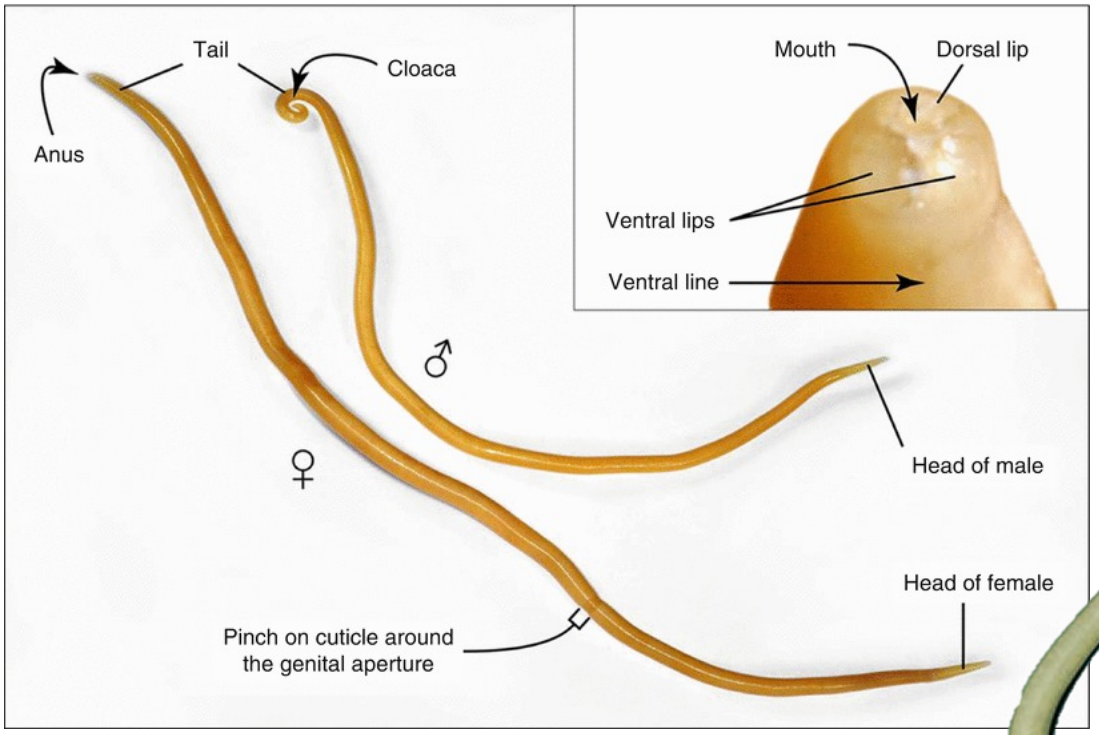
Organism: General information

- Common name: **pig roundworm**
- Number of chromosomes: 2n = 16
- Genome size: 309Mb
- Infects around 1.2 billion people.
- Cause major production loss in pigs.



Organism: Geographic distrubution

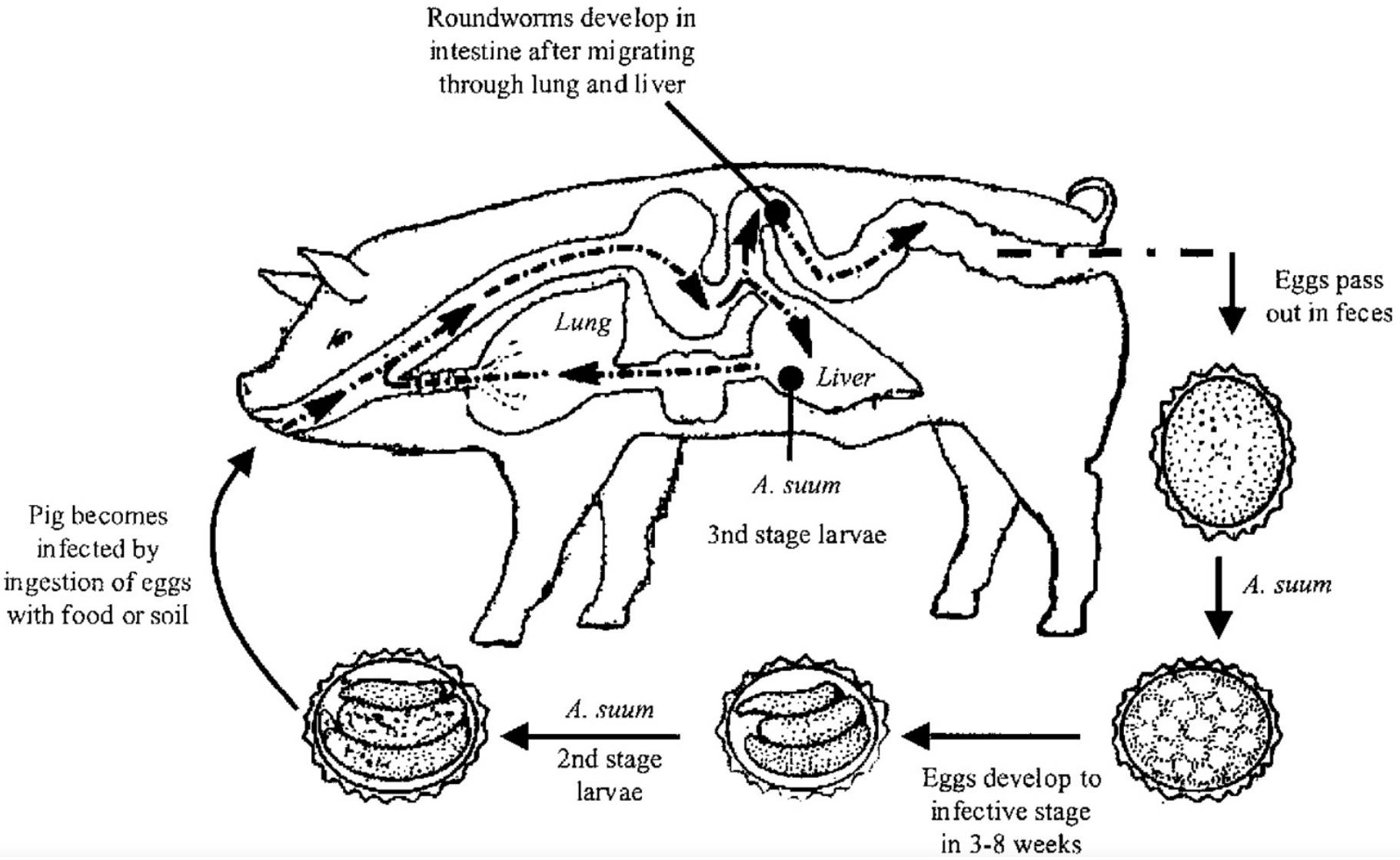
Organism: Physical characteristics



Female: 20 – 40 cm

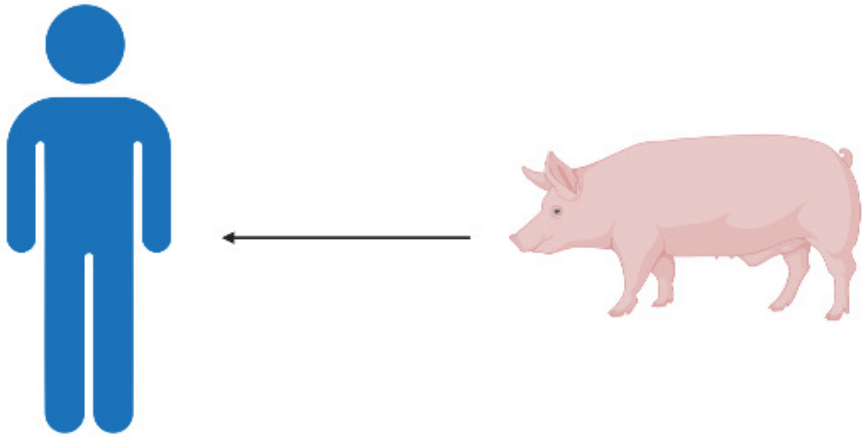
Male: 15 – 30 cm

Organism: Life cycle



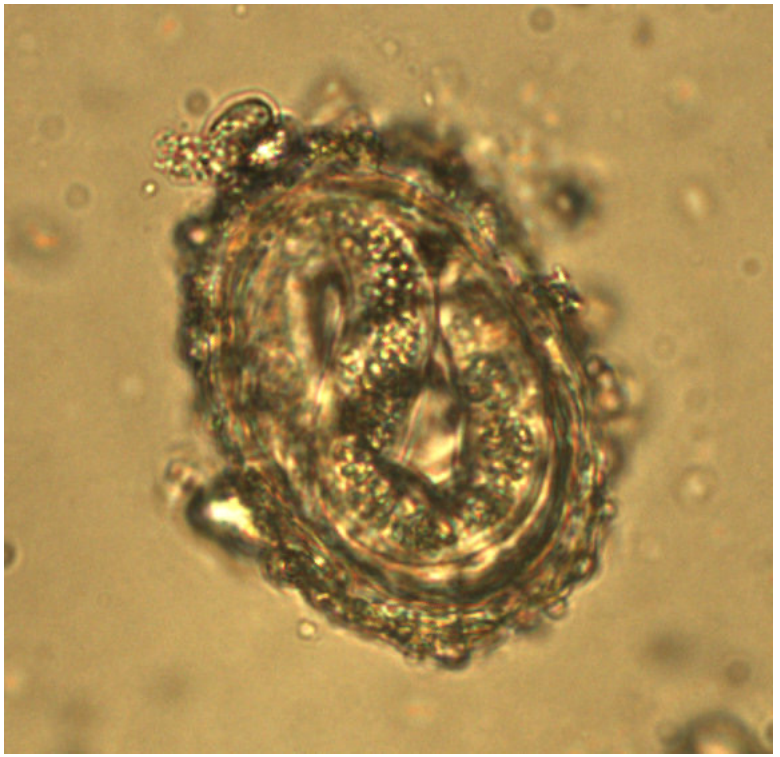
Organism: Significance

- The Ascaris-swine modle makes it possible to study the parasite, its relationship with the host and ascariasis at the molecular level.
- Cause nutritional deficincy impaired with physical and coginitive development and in severe cases it might lead to death.
- Pneumonia, Hepatits in both humans and pigs.
- ill-thrift in pigs.



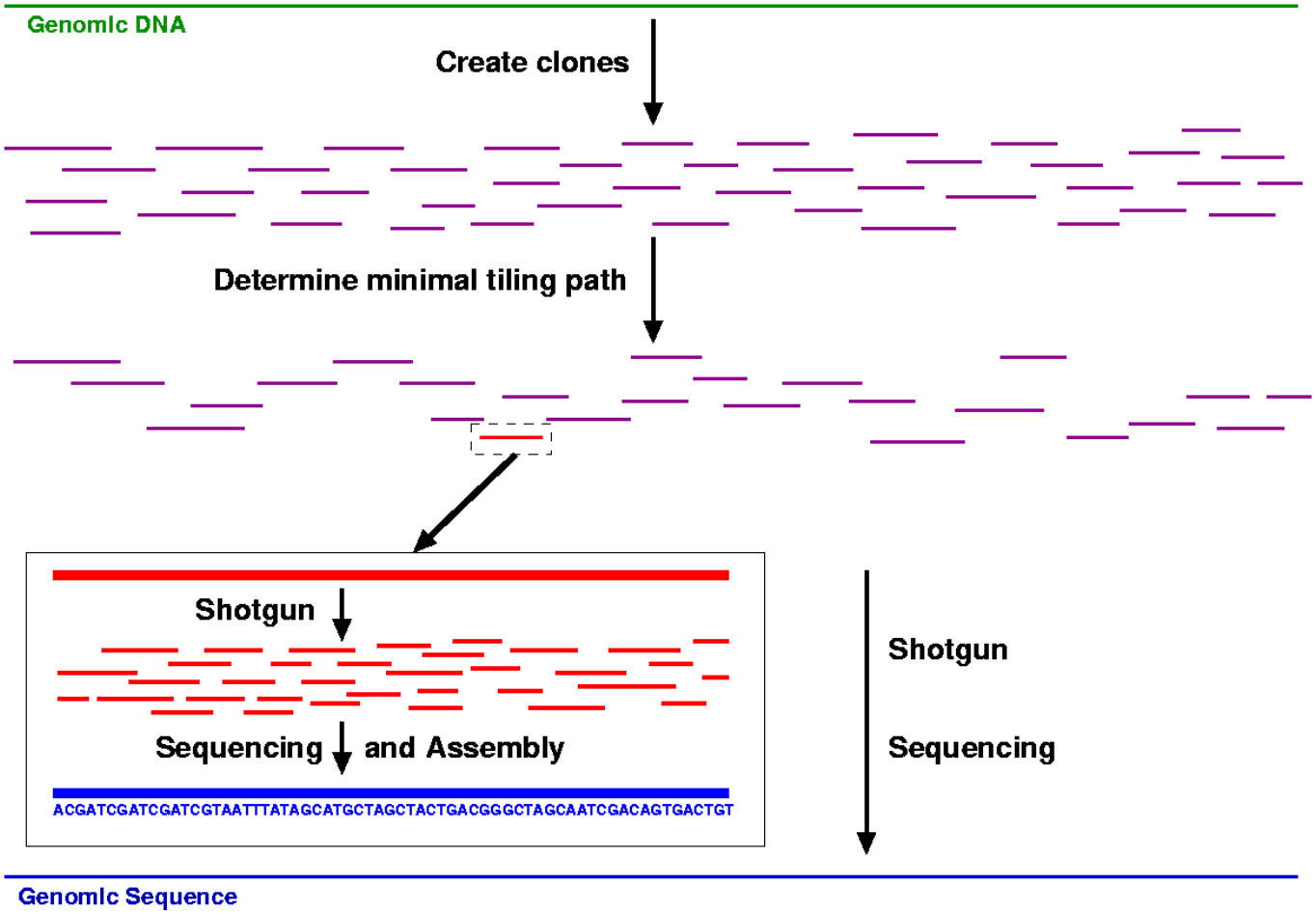
Sequenced sample info

Sequenced sample was obtained from the productive tract of a single female adult.



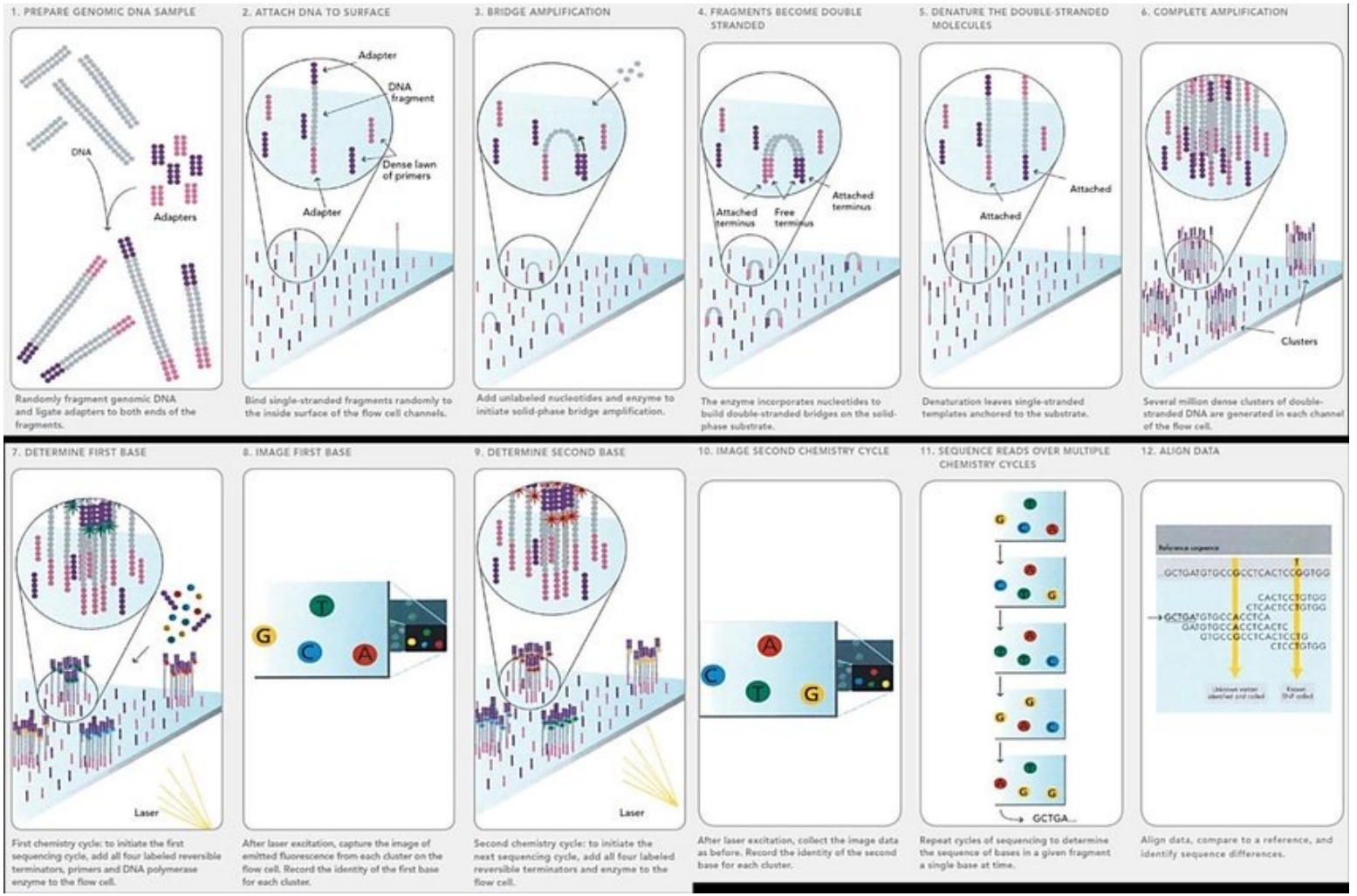
Sequencing strategy

- The used sequencing strategy was whole genome shotgun



Sequencing method

- The used sequencing method was illumina

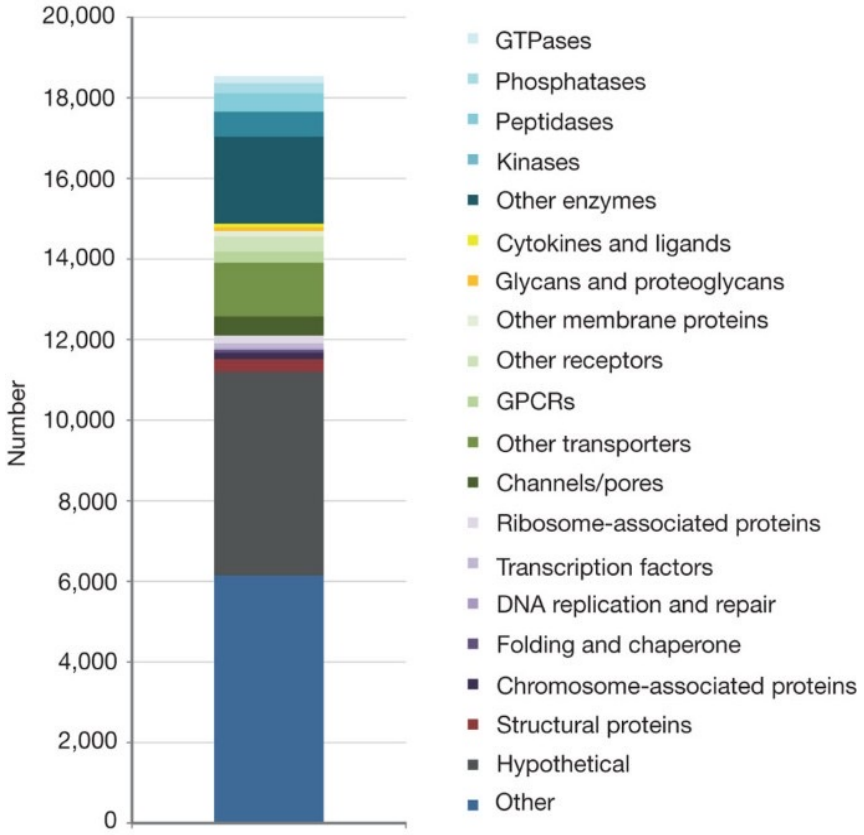


Genome assembly

Method of assembly	SOAPdenovo
Assembled scaffolds	273 Mb
Coverage	80 fold
N50 length	407 Kb
N50 contig	1618 Kb
DNA transposons	91
LTRs	283
LINEs	118
SINEs	10

Interesting genome outcome

- Has longer genes in comparison with other roundworms.
- There is a high synteny ~15% between *A.suum* and *B.malayi.*
- has low repeat content = 4.4% of the total assembly
- Encode about 18500 protein coding genes
- The secretion of *A.suum* is rich in **peptidase** which gives it the ability to degrade and penetrate host tissues.



Questions

- What is the common name of *A.suum*?
- What component of *A.suum* secretion gives it the ability to penatreat and degrade the host tissue?

thank you!