

The Genome Project of *Taenia solium*

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A consortium of key laboratories at the National Autonomous University of Mexico is carrying out a full genomic project for *Taenia solium*. This project will provide powerful resources for the study of taeniasis/cysticercosis. The nuclear DNA content estimated through cytofluorometry on isolated cyton nuclei was of about 270 Mb. Two probabilistic calculations based on shotgun sequenced genomic clones, resulted in size estimates for the haploid genome of 120–140 Mb. A combined strategy with 454 and capillary sequencing is under process. So far, we have achieved 10X coverage by 454 pyrosequencing and 3.6X coverage by capillary sequencing. Results suggest that *T. solium* genome is not highly repetitive (<7%). One small 53 bp tandem-repeat and different tetranucleotide repeats represented 0.5% and 4.5% of the genome, respectively. Current assemblage still shows tens of thousands contigs, however, estimates suggest that 90% of the genes are already included.

Besides genomic sequencing, more than 34,000 ESTs have been obtained: 14,113 from adult cDNA libraries and 9,157 from larval libraries, which have been made public through GenBank. Additional 10,000 5' end sequenced ESTs from a larval full-length cDNA library are already available. Unique genes were identified by clustering all EST-fragments with an assembler (minimus). We have identified around 7,000 "genes", some of them are highly expressed in both adult and larvae stages. Thus, there are 349 "genes" with 10 or more sequences that account for 50% of all transcripts. Approximately one third (2,038) of the 7,000 genes have a significant match in SwissProt and about 27% of the genes have no match in SProt + TREMBL, and could constitute new genes.

The consortium for the *T. solium* genome project wishes to use this International Congress of Infection Diseases to make a worldwide call for collaborative research. This project is supported by a special grant IMPULSA-UNAM.

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Low Degree of Genetic Diversity Within and Among *Taenia solium* Cysticerci from Natural Infected Pigs of Central Mexico

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Taenia solium is responsible for porcine cysticercosis, and human taeniasis. The parasite constitutes a serious public health problem in endemic areas of Latin America, Asia and Africa. The eggs can infect humans, resulting in cysticercosis or neurocysticercosis. Neurocysticercosis is a serious disease resulting in high morbidity and, in some cases, death. Random amplified polymorphic DNA markers (RAPDs) was employed to assess genetic variation within 13 *T. solium* muscle cysticerci collected from 14 naturally infected pigs. Using six different random primers and a total of 181 cysticerci, 88 different loci were amplified, among which 77 (85%) were polymorphic between pigs and from 0 to 24% within pigs indicating the polymorphism of the population. The phenogram grouped the cysticerci population into 8 major clusters with low differences in the genetic distances among and within pigs' parasites (ranged from 0.78 to 1.00) mainly grouping according to the pigs' origins.

Genetic similarities amongst the cysticerci from different pigs were estimated using the Jaccard algorithm. A cluster analyses were performed using UPGMA and neighbor joining methods. Principal components analysis was also employed. The high cophenetic correlation coefficient obtained for the Jaccard algorithm and the UPGMA clustering method corroborated small variability observed of isolates from Central Mexico.

Both, the association (0.0 to 0.089) and the genetic diversity indexes (0.009 to 0.073), support the idea that DNA diversity is mainly due to a recombination process. Diversity, possibly due to different infection within pigs was also found albeit exceptionally.

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Intestinal Parasitic Infections Among Children and Their Medical Staff in a Romanian Pediatric Care Unit

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Parasitic diseases represent an important public health problem. Digestive parasitosis are characterized by high prevalence and a variety of clinical manifes-