The parasite *Onchocerca volvulus* poses serious health and socio-economic risks to individuals living in endemic regions. Currently, there is no vaccine available to prevent this disease, and the available chemotherapy does not eliminate adult infection. To date, very few stage-specific expressed genes have been cloned or sequenced from *O. volvulus* due to a paucity of parasite material to construct high quality cDNA libraries. We have constructed a cDNA library from 6000 *O. volvulus* molting L3 larvae. The primary library contains 1.1 million independent clones, an average insert size of 1200 base pairs, and 10% non-recombinants. The library has been characterized by expressed sequence tag (EST) analysis of over 1200 randomly selected clones. EST results indicate that the library is of high quality with only 0.01% *E. coli* contamination and less than 13% rRNA sequences. Comparisons to EST and gene sequences present in the GenBank databases indicates that the library contains 54% novel genes not yet seen in any other filarial cDNA libraries. This suggests that during the molt from L3 to L4, many unique genes are being expressed. Since the L3 to L4 molt is crucial to the completion of the parasite life cycle within the human host, genes that are required for this process may be ideal vaccine candidates or drug targets. A survey of novel genes in the molting L3 cDNA library includes unique collagens, transmembrane proteins, antioxidants, thiolesterases, and other clones which do not match the sequences of any genes with known function. Currently, this library is being immunoscreened using sera from both infected and putatively immune patients to isolate immunogenic clones for further characterization.

Jean-Marc

X540 USE OF A SIMPLE ENTOMOLOGICAL METHOD FOR DETECTION OF ONCHOCERCIASIS INFECTION IN THE ONCHO-FREED ZONES. Yaméogo L*, Toé L, Hougard JM, and Boatin BA. Onchocerciasis Control Programme in West Africa, Ouagadougou, Burkina Faso; Onchocerciasis Control Programme, Entomological and Insecticide Research, Bouaké, Cîte d'Ivoire.

One of the major challenges of the Onchocerciasis Control Programme in West Africa (OCP) is to place the 11 Participating Countries in a position to be able to take over its residual activities when the Programme comes to an end in 2002. At that time, epidemiological surveillance and ivermectin treatment will remain the residual activities to be implemented by the countries. To ensure the success of these activities, the Programme must make available to the countries efficient tools and methods which are acceptable to the populations, inexpensive and easy to use. It is to this end that for the epidemiological surveillance of onchocerciasis, different tools are being tested to replace the skin snip method which is becoming less and less acceptable to the populations. As an addition to these techniques which are applicable to man, an entomological tool which is based on molecular biology allows for the assessment of the infectivity level of blackflies, the vectors of onchocerciasis, in a given area. In this exercise, the catching of blackflies is carried out by trained villagers, and the presence of the infection in the blackfly populations is assessed through the DNA technique. The first results obtained at the molecular biology laboratory of the Programme show a good correlation between the infectivity levels obtained through the common dissection method and those assessed through the DNA technique. It is concluded, that this molecular biological technique for assessing infectivity levels in flies without dissection could be a viable addition to the tools for epidemiological surveillance.

541 PROTEIN (TCTP) HOMOLOGUE FROM THE FILARIAL PARASITE *BRUGIA MALAYI*. Rao KV*, Sabarinathan R, Ravi V, Narayanan RB, Kaliraj P, Jayaraman K, Raghavan NK, and Scott AL. Centre for Biotechnology, Anna University, Chennai (Madras) India; and Department of Molecular Microbiology and Immunology, SPH, Johns Hopkins University, Baltimore, MD.

As part of the WHO sponsored filarial EST (Expressed Sequence Tags) project several genes were sequenced from the *Brugia malayi* L4 cDNA library (JHU93SL-BmL4). The sequences were analysed and one of the clones showed significant homology with the translationally controlled tumor protein and has been named as BMTCTP. The clone BMTCTP was sequenced completely on both the strands. The BMTCTP sequence had 67.4% similarity with *C. elegans* TCTP at the amino-acid level. BMTCTP contained an insert of 739 bp with an ORF of 543 nucleotides encoding 181 amino acids. The 5' end 22 nucleotide conserved sequence SLI was located 40 bp upstream of the putative start codon "ATG". The 3'end UTR was of 119 bp in length contained Poly A tail with possible ploy adenylation signal "gataaa" located 13 bp upstream of Poly A sequence. A homologue of BMTCTP was also identified from Wuchereria bancroffi adult female cDNA library by screening with a DNA probe, but it was of partial length due to the presence of internal restriction site. By searching *Brugia malayi* dbEST it was found that the transcripts of BMTCTP are present in all the stages of the parasite but it is not known about the function and regulation of expression of this gene. The gene may be probably involved in the regulation of cell proliferation as the filarial parasite undergoes several moultings before maturation in to the adult. It was shown that recombinant TCTP from U937 cell line caused the IgE dependent histamine release from basophils. Hence this gene might play a role in the modulation of host immune response. Thus characterisation of this gene would facilitate the understanding of the biology of the host-parasite interactions. In order to characterise th is protein the coding region corresponding to 181 aa was amplified with gene specific primers and cloned at the BamHI (5') and EcoR1 (3') sites

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Disney's Coronado Springs Resort
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