BQ-026
TWO GROUPS OF *TRYPANOSOMA CRUZI* ARE DEFINED BY TWO INDEPENDENT NUCLEAR MARKERS

Souto, R. P.1; Fernandes, O.2; Macedo, A.M.3; Breniere, S.F.4; Sturm, N.5; Campbell, D.A.5; Zingales, B.1
1. Departamento de Bioquímica, Instituto de Química, Universidade de São Paulo; 2.Departamento de Bioquímica e Biologia Molecular, Fundação Oswaldo Cruz e Departamento de Patologia, UERJ; 3. Departamento de Bioquímica e Imunologia, Instituto de Ciências Biológicas, UFMG; 4.Departamento de Parasitologia, La Paz, Bolivia; 5.Department of Microbiology and Immunology and Molecular Biology Institute, UCLA, School of Medicine, USA.

Studies on the population genetics of *T. cruzi* revealed substantial variability of these organisms regarding the isozyme genotype, and the main conclusion of these analyses is that the population structure of the protozoa is clonal rather than sexual. Other molecular methods such as schizodemes and RAPD also defined highly variable groups. In order to analyze the genetic diversity in *T. cruzi* , we applied two independent nuclear genes that have proven to be useful as molecular markers of 1) evolution in most cell types - the ribosomal RNA genes and 2) genomic variation in trypanosomatids - the mini-exon gene. The measure of diversity among *T. cruzi* isolates consists of 110 bp or 125 bp amplification products derived from the 24Sa rRNA gene using the same pair of primers (Souto & Zingales, 1993), and to the mini-exon gene non-transcribed spacer region (Murthy et al., 1992) that shows 40% divergency between the two groups.

A dimorphism in the *T. cruzi* mini-exon non-transcribed region is able to cluster 66 isolates in two distinct groups (1 and 2) that correlates with the ribosomal DNA dichotomy in 57 samples. In a portion of the samples (9), both the 125 and 110 bp products derived from the 24Sa rRNA gene were amplified (group 1/2). Since 6 of these samples were clonal lines, the possibility of mixed population is ruled out. These nine samples were typed as mini-exon gene group 1. Analysis of these two independent nuclear markers and confirmatory RAPD data suggested the division of *T. cruzi* isolates into two major groups. The presence of the rRNA gene group 1/2 calls the attention to the possibility of gene flow in these parasites.

This research is sponsored by the Burroughs-Wellcome Fund, CNPq and FAPESP.

BQ-027
CONSTRUCTION OF "TCRUZIDB", AN INTEGRATED GENOME DATABASE FOR *TRYPANOSOMA CRUZI*

de Miranda, A. B.; dos Santos, R. and Degrave, W. M.
Department of Molecular Biology and Biochemistry - Oswaldo Cruz Institute - FIOCRUZ - Avenida Brasil 4365, Manguinhos, Rio de Janeiro, RJ.

In order to construct a *T. cruzi* genome database, ACeDB software (version 3.2 but update to 3.7 or the new 4.x version is planned in the near future) has been installed on a SGI Challenge L server, and data on the genome project are currently being entered. All *T. cruzi* sequences present in GenBank and EMBL have been ordered in classes, after checks for consistency and screening for redundancy. Class "antigens" contains currently 42 entries (70,656 bp); class "housekeeping genes" contains 113 entries (183,209 bp); class "minicircles" contains 9 entries (7.838 bp); class "repetitive sequences" contains 40 entries (21.713 bp); class "structural RNA" contains 22 sequences (20,540 bp) and class "other sequences" (probes, unidentified sequences, etc.) contains 13 entries (10,100 bp). Also, data on *T. cruzi* codon usage, participating laboratories in the genome project, bibliography, and chromosome allocation of sequences, when available, are being entered.

In parallel, a WWW server (http://gene.dbbm.fiocruz.br) has been organized and data on the *T. cruzi* genome project are being displayed as they are becoming available. Furthermore, a *T. cruzi* mail service (tcruzi-l@gene.dbbm.fiocruz.br), as a moderated list, was set up to promote exchange of information and discussion on the parasite genome project. Subscription requests to the list may be sent to listserv@gene.dbbm.fiocruz.br.

Access to the WWW server is already available, whereas the first version of TcruziDB is expected to be released by October 1995. Other ways of making the genome data available are under discussion.

This research is sponsored by UNDP/World Bank/WHO Special Programme for Research and Training in Tropical Diseases, FINEP and Fiocruz PAPES Program.