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Human nutritional status as a measure of the impact of livestock disease control

Improving the health of livestock raised by small-scale farmers ameliorates nutritional as well as economic hardships in developing countries. By implementing measures to control cattle diseases such as East Coast fever, farmers earn much-needed cash income, most of it from sales of surplus milk produced by increasing livestock survival and productivity. Just as important, however, is an expected improvement in the nutritional status of farm households that invest in livestock disease control. The results of a collaborative study conducted by scientists from ILRAD, the International Livestock Centre for Africa, based in Addis Ababa, and the Kenya Agricultural Research Institute indicate that changes in household nutritional status are reliable indicators of the effects on communities of improving control of animal diseases.

Staff of ILRAD's Socioeconomics and Environmental Impact Program are determining and quantifying the effects of parasitic livestock diseases and their control on animal productivity, rural communities, the environment, and general agricultural and economic development in Third World countries. Computer-based, analytical tools are being developed, for assessing the impacts of the application of more efficacious disease-control methods, such as innovative 'subunit' vaccines against protozoan parasites or the animal diseases they cause. These advanced disease-control methods are under research at ILRAD**,** which works in collaboration with research institutes in developed countries and with national agricultural research systems in Africa and other developing regions.

The more accurate assessments ILRAD staff are making of the impacts of animal diseases and their improved control are urgently needed. Without such information, policymakers are unable to determine optimal disease control strategies for different areas or to set judicious priorities in agricultural research.

Enhancing decision-making in animal disease research and control is important. In the last decade, the industrialized nations steadily reduced their support for long-term research on agricultural problems of developing countries. This decline in funding is expected to continue

throughout the 1990s and beyond. With fewer resources to support it, livestock disease research and control work must be targeted to topics and methods that hold the greatest potential for generating broad-scale, equitable, cost-effective and sustainable production increases. Better information is needed to pinpoint these highest-potential areas.

To increase agricultural production and enhance standards of living in the developing world, smallholder production systems will have to be intensified. This will occur largely by applying technical innovations and increasing mixed crop and livestock farming. Success of the latter will depend on an ability to control parasitic diseases of ruminant livestock endemic in Africa and much of the developing world. Two of the most important of these are trypanosomiasis, known as sleeping sickness when it occurs in people, and theileriosis, commonly known as East Coast fever.

Farm households must make nutritional as well as economic progress to unlock the rural potential of developing countries. A productive countryside—able to strengthen livelihoods and to spur economic development—rests largely on access to sufficient quantities and qualities of food.

Keeping livestock is a common way for small-scale farmers to secure reliable access to food. It often is also a catalyst to a better life: livestock rearing augments not only the nutritional status and productivity of rural households, but also the productivity of their crop farming.

Assessing the nutritional impact of animal disease control

The conventional way to measure the impact of an animal disease or its control on the well-being of a community is to estimate the economic costs of the disease—for example, the numbers of animals killed and calves lost in abortions, losses in milk and meat production, and the costs of implementing disease control measures—as well as the benefits of controlling the disease, such as increases in production of milk, meat, draught power and manure.

Economic measures, however,—which are often expressed in benefit: cost ratios, rates of return or net profit and income—tell only part of the story regarding the well-being of small holders. With colleagues from the Kenya Agricultural Research Institute (KARI), ILRAD and ILCA scientists carried out studies one conducted in the high rainfall region of the Kenya coast and the other in the temperate highlands of Kenya's Uasin Gishu Plateau—which suggest that improved control of livestock diseases leads to improvement in farm household diet and nutrition. The studies also show that such links may be used in estimating the effects of implementing alternative methods of livestock disease control. The addition of such non-economic indicators to the conventional economic ones will greatly enhance impact assessments.

At the Kenya coast, where commercial cattle-keeping is a relatively recent enterprise, farm incomes are small. Most of the cattle are of low-producing indigenous zebu breeds, although more productive exotic-zebu crossbred animals are being kept in zero-grazing units as part of a National Dairy Development Project (NDDP). The study found that livestock keepers, particularly members of the NDDP, had higher incomes and were better nourished than the general population. All households in this study area reported that animal disease is a major constraint to increasing both dairy production and dairy product consumption.

In the highland study site, dairying is a major farm enterprise. The cattle kept in this cool-climate area are predominantly crossbred. Dairy production in the area is practised by large-, medium- and small-scale farmers alike. The study results indicate that smallholders are the group likely to benefit most, both economically and nutritionally, from improved animal health and consequent animal survival. (Small-scale farmers withhold a larger proportion of the milk produced on the farm for household consumption than larger-scale farmers.)

Support for research on Third World agricultural problems is eroding as food production per capita continues to decline in 75 developing countries. More than 700 million people have access to insufficient food to lead healthy, productive lives. More than 180 million children are underweight; as many as 500,000 go blind each year due to vita min A deficiency. Besides causing suffering and death, lack of micronutrients cuts deeply into the productivity of poor nations.

The outlook for Africa and Asia, economically the most vulnerable regions of the world, is particularly, bleak. One in every four Africans and Asians is too poor to meet his or her basic dietary needs reliably. In sub-Saharan Africa, where the population is expected to grow at three per cent a year and food production at less than two per cent, a food shortage of 250 million tons is expected by the year 2020.

(*Figures taken from the February 1994 IFPRI Report and March 1994 Food Policy Statement, International Food Policy Research Institute, Washington; D.C.)*

In other studies carried out in collaboration with KARI in Kaloleni Division, at the Kenya coast, ILRAD and ILCA staff obtained comprehensive data on the current livestock production and welfare of farm households. Information collected in the future will be compared with these baseline data to assess the impacts of different kinds of interventions made to better control livestock diseases such as East Coast fever.

The results of the KARI/ILRAD/ILCA studies highlight the importance of including nutritional status when assessing the impacts of disease control on rural communities. ILRAD is applying this knowledge in its research. Nutritional parameters, for example, have been included in a farm-level simulation model developed to compare the probable impacts of using alternative disease-control interventions.

This article is based on research by Rebecca Huss-Ashmore, a Visiting Scientist at ILRAD now at the University of Pennsylvania; William Thorpe and Gary Mullins, animal scientist and agricultural economist, respectively, working for ILCA at the Kenya coast in a collaborative project with KARI; John Curry, a former ILRAD anthropologist; and Adrian Mukhebl, an ILRAD economist.

Better diagnosis of trypanosomiasis

Effective management of an animal disease problem depends on accurate diagnosis at both the individual and the herd level. Parasitological detection methods are usually employed to diagnose African animal trypanosomiasis. Most of these conventional diagnostic methods involve examination of peripheral blood for the presence of trypanosome parasites. The sensitivity of these techniques is too low to identify all infected animals. Inability to detect parasites, even in animals suffering acute disease, makes diagnoses inaccurate.

Knowledge of the morbidity of animal trypanosomiasis has been poor because of these diagnostic difficulties. Moreover, veterinarians and disease control workers often institute chemotherapeutic intervention on the basis of clinical signs rather than parasite detection. Thus, infected animals exhibiting no clinical signs of disease act as reservoirs of infection for clean animals in a herd.

Trypanosomes that are undetectable in peripheral blood may be sequestered in several organs of an infected host, such as the spleen, lymph nodes, bone marrow and liver. Successive variable antigen types (VATs) in these parasite populations are released in the tissue fluids as the immune system of the animal host eliminates one trypanosome population after another, each population being distinguished by a different VAT. Some of the antigens released occur in a single trypanosome species. Detection of these species-specific antigens provides evidence of infection with a particular parasite species. Several antigen-trapping ELISAs (enzyme-linked immunosorbent assays) developed at ILRAD work in this way to diagnose trypanosomiasis.

The assays are known as 'sandwich ELISAs': trypanosome species-specific monoclonal antibodies are used to capture circulating trypanosome antigens in the serum of infected hosts. The captured antigen is revealed by introduction of the same monoclonal antibody labelled with horseradish peroxidase (HRPO), which binds to free antigenic epitopes of the immobilized antigen. The labelled antibody is subsequently revealed by the activity of the HRPO on its substrate, which causes the colour of the introduced chromogen to change. ILRAD has developed three such assays to detect antigens of the *Trypanosoma congolense* and *Trypanosoma vivax* species and the *Trypanozoon* subgenus.

Some of 25 technicians trained in ILRAD courses in use of an IAEA/FAO ELISA kit for diagnosing trypanosomiasis. This improved diagnostic kit is based on reagents developed over several years in the course of ILRAD's trypanosomiasis research. The ELISAs provide direct evidence that an animal has a current infection with a species or mix of species of trypanosome parasites. The tests are simple to perform, generate reproducible results and can be applied in the field.

Introduction of the antigen-trapping ELISA, which distinguishes infections with *Trypanosoma brucei, T. congolense* and *T. vivax* in mammalian blood, has greatly improved the ability of diagnosticians to identify trypanosome-infected animals. An early experiment conducted to compare the efficacy of the conventional and new diagnostic techniques indicated that the antigen-trapping ELISA was at least four times more sensitive than the buffy coat technique in detecting *T. congolense* infections in animals.

The diagnostic utility of ILRAD's ELISAs has been independently tested in laboratories in ten African countries: The Gambia, Ghana, Kenya, Mali, Senegal, Sudan, Tanzania, Uganda, Zambia and Zimbabwe. This validation exercise was sponsored by the Netherlands Government and directed by staff of the Joint Food and Agriculture Organization/International Atomic Energy Agency Division of Nuclear Techniques in Food and Agriculture, in Vienna. The validation demonstrated that ILRAD's antigen-trapping ELISAs are both sensitive and reliable in most circumstances. Results produced using the tests have a sensitivity and specificity greater than those generated by routine parasitological techniques.

The African laboratories that participated in the validation are now using the antigen-trapping ELISAs to monitor the effectiveness of their national and regional tsetse and trypanosomiasis control programs. To increase expertise in use of the ELISAs in Africa's national agricultural research systems, ILRAD has conducted two courses, one in 1992 and one in 1994, to train 35 trypanosomiasis research and control staff from 23 African countries. Most of the trainees are technicians and research working in university or central veterinary laboratories where the diagnostic test is being evaluated.

After a final FAO/IAEA meeting was held, in 1992, to review results of the field validation of ILRAD's antigen-trapping ELISAs, a scientist from IAEA's Seibersdorf Laboratory (Vienna) spent two months at ILRAD learning procedures used to raise the monoclonal antibodies that are the bases of the assays. With this transfer of technology, staff at IAEA are now able to generate all the reagents employed in the ELISAs.

Following the planned establishment of a hybridoma production system in the Vienna laboratory, IAEA will begin to supply these reagents to the African laboratories using this technology so that they can monitor their trypanosomiasis control programs. ILRAD scientists will continue to help staff of Africa' national agricultural research system to overcome problems that may arise in applying the ELISAs in the field.

This article is based on work and report by Rachel Masake, an ILRAD scientist.

Novel vaccination strategies against protozoan parasites

In November 1993, ten international scientists at the forefront of research on vaccines for parasitic diseases joined ILRAD scientists in a four-day workshop. The participants examined current and potential applications of recent advances in immunological research to vaccine strategies for protozoan organisms. The latter include two parasites studied at ILRAD that debilitate and kill livestock in tropical countries: *Theileria parva,* the cause of theileriosis (East Coast fever), and trypanosomes, the cause of African animal trypanosomiasis. Among the topics under review were a new understanding of the events that induce parasite-specific cytotoxic T lymphocytes (CTL) to poliferate in an infection, perturbatious of the immune system related trypanosome infections, the role of T-cell subpopulations in development of host immunity to trypanosomiasis, and the role cytokines play in both the control and the pathology of parasitic infections.

East Coast fever

Much discussion centred on the potential of a novel East Coast fever vaccine under development at ILRAD, which is considered very promising. This vaccine is based on the dominant antigen of the *T parva* sporozoite surface. The antigen, designated p67 and produced by expression of the gene in *Escherichia coli*, has been used successfully to immunise cattle against experimental challenge. Further research into the p67-antigen vaccine and continuing immunisation trials are being vigorously pursued.

Participants discussed the merits of working towards development of a multiple-antigen vaccine. ILRAD experiments have provided direct evidence that CTL play a major role in clearing *T. parva* from immune cattle under challenge. A successful vaccine that will safeguard against disease caused by breakthrough infections will thus most likely require antigens from both the sporozoite and the schizont life-cycle stages of *T. parva*. Much effort at the Laboratory is focussed on identifying parasite-specific CTL and defining the requirements for inducing CTL responses in cattle.

The workshop participants reviewed recent results in research on bovine MHC (major histocompatibility) molecules and compared two methods developed for identifying antigens recognized by CTL: peptide stripping and random screening of complementary DNA. It was agreed that tumour cells were better models for the search for CTL epitopes than the relatively crude techniques used to isolate viral antigens.

Although these new technologies have to date yielded only a few antigens with vaccine potential, ILRAD is in an excellent position to use these methods to advantage. As stated, CTL have been shown to protect animals against *T. parva;* furthermore, ILRAD has already established technologies for isolating peptides and screening complementary DNA and the institute has on-going collaborations with leading laboratories in this research area. Use of these techniques is also attractive because there are estimated to be fewer than 4,000 schizont transcripts and because new developments in bovine MHC studies are expected to facilitate the antigen search.

ILRAD will explore development of a vaccine based on the p67 antigen of *T. parva* with a commercial partner. In general, ILRAD's role in animal vaccine development is to conduct research leading to identification of parasite antigens with promising vaccine potential and subsequently to present the candidate antigens successfully in the animal host. Producing a new vaccine in large quantities and maintaining its quality will be the responsibility of the commercial partner. Molecular modeling could be used to ensure quality control. This is expensive work, however, and some participants believed that unless there were a reasonable three-dimensional structure of a candidate antigen, modeling would be unwarranted.

Trypanosomiasis

If a single mechanism controls trypanosome numbers in an infection, an intervention to stop the development of disease might usefully complement an anti-parasite vaccine. Differences in responses to infection made by trypano-susceptible Boran and trypanotolerant N'Dama cattle were discussed. Of factors likely to be responsible for inducing pathology in infected trypano-susceptible Boran animals, parasite load and a failure of the Boran antibody response to mature through isotype switching were considered productive areas for further research.

It was noted that an endocrinological failure in trypanosomiasis resembles that in malaria, where *Plasmodium* antigens disturb the insulin signalling pathway. Trypanosome antigens may induce a similar perturbation, resulting in pituitary dysfunction. In collaboration with laboratories employing reliable *in vitro* assays of endocrine function, ILRAD will continue to investigate the possibility that cytokines or hormones are responsible for the metabolic and physiological disturbances in trypanosomiasis.

Massive disturbances of the immune system occur in both trypanosomiasis and East Coast fever. Few if any investigations are being conducted on the role cytokines may play in causing such large disturbances. ILRAD is in an excellent position to resolve this question. Investigations of cytokine activity would help differentiate harmful affects that may be induced in the host by cytokines, particularly tumour necrosis factor, gamma-interferon and interleukin-1.

The cause of the striking differences between Boran and N'Dama cattle in immunoglobulin responses to trypanosome infection may lie in differential immunological memory as well as isotype switching. The differences may be due to the kinds and amounts of cytokines produced by T lymphocytes and other regulatory cells of the host. Participants discussed the potential of exploiting the trypanosome cysteine protease ILRAD scientists have identified and isolated as a tool to investigate disturbances in the immune response. It is possible that the presence of this molecule in the blood of the host is responsible for the development of disease in susceptible infected animals.

Both diseases

Participants reviewed the experimental advantages of using cattle versus mice in research on vaccines against livestock diseases. Mice—particularly 'knock-out' mice, which have been depleted of a given gene, and thus the product of that gene—have proved excellent models for identifying protective immune responses to parasite infection, and for that reason will continue to be used, especially in trypanosomiasis research. Although eliminating all cells of a given type in cattle is also desirable, this remains difficult to accomplish. In spite of this, cattle experiments are particularly informative at ILRAD due to the Laboratory's access to large numbers of good-

quality cattle of defined genotypes, including monozygotic and chimaeric twins produced on the Laboratory's cattle ranch. ILRAD will thus continue to exploit this comparative research advantage to the full.

A preliminary understanding of the role played by gamma/delta T cells in trypanosome and *T. parva* infections is being obtained by research conducted at ILRAD and elsewhere. A thorough understanding of the function of these immune cells is needed because they occur in significantly large numbers in calf spleens, and it is young animals that will be the main target for vaccination. It was speculated that gamma/ delta T cells play a role in enabling young cattle to tolerate or control parasite infection and to develop immunity without developing disease. Low numbers of natural killer cells are also present in cattle blood and are readily activated by cytokines.

A brief discussion was held on the plastic nature of immune responses— that is, that different animals employ different immune cells and mechanisms to protect themselves against *T. parva* and trypanosome infections. In outbred populations, this phenomenon (detected in cell transfer experiments) may be due to the occurrence of parasite epitopes that differ slightly in quantity or quality from one infected animal to another. It was agreed, however, that little merit existed in ILRAD's complicating its investigations of protective immune responses with concerns about plasticity. Rather, ILRAD's approaches to vaccine development will focus on major immune responses in target animal populations and the parasite antigens that elicit them.

Finally, the workshop participants emphasized that a search for protective antigens requires a better under standing of the cell biology of the parasites. This research produces additional information about the parasites and their interactions with the host. Analyses of data obtained from cell biology research help reduce the number of antigens that must be screened for biological characters and may help reveal antigens likely to elicit protective immune responses.

This article is based on workshop reports by ILRAD scientists Tom Dolan, Rob Skilton and Maarten Sileghem. Declan McKeever Is editing the proceedings of the workshop and commented on a draft of this article.

Developing nucleic acid-based methods for typing class II MHC in cattle

The protozoan parasite *Theileria parva* causes theileriosis, an acute and usually fatal lymphoproliferative disease of cattle in Africa, where it is commonly known as East Coast fever. A major goal of ILRAD's research program is development of an improved vaccine that will protect cattle from this parasite.

Significant progress has been made towards achieving this goal (see the July 1992 issue of this newsletter). Administration of a recombinant form of a major surface antigen of the sporozoite stage of the parasite has been shown in experiments to protect cattle against subsequent challenge with normally lethal doses of *T. parva*. lLRAD is developing his antigen for delivery in a first-generation 'subunit' vaccine, which is based on one or more antigenic parasite molecules rather than the whole parasite.

It is well known that the quality of an immune response to infection with an intracellular parasite depends greatly on molecules encoded by genes located in an area of the mammalian genome known as the major histocompatibility complex (MHC). T lymphocytes of the host animal recognize antigens only when these are wedged in the binding clefts of 'self' MHC molecules located on the surface of antigen-presenting cells. The ability of a given parasite antigen to elicit an immune response is likely to be related to the antigen's ability to bind to the MHC molecules expressed by an individual animal.

Two classes of MHC exist and both classes are polymorphic, that is, molecules of each class vary from one individual animal to another. It is possible that MHC polymorphisms within outbred populations of cattle will influence the efficacy of a subunit vaccine in the field. This possibility has led ILRAD scientists to search for reliable techniques with which to type the MHC of cattle.

The typing of bovine class I MHC molecules is in an advanced state. This work has greatly facilitated the characterization of *T. parva*-specific cytotoxic T-cell responses in cattle. In contrast,

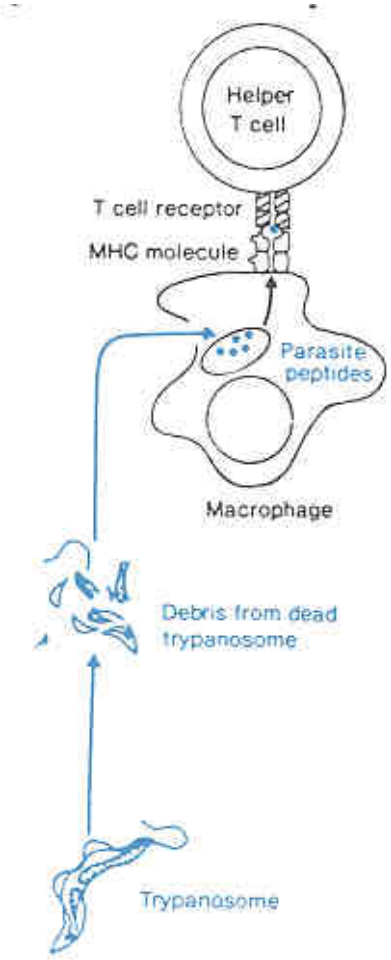
available methods for characterizing bovine class II MHC molecules—the MHC class that will influence the efficacy of a p67-based vaccine—have been tedious to use and unsuitable for non-specialized laboratories and field conditions. Recently developed DNA based typing methods have many advantages over the older methods. The availability of these new methods has made development of a simple nucleic-acid-based system for bovine class II MHC typing and characterization a priority for scientists in ILRAD's vaccine development program.

Since 1991, ILRAD has collaborated with the Roslin Institute, in Edinburgh, on a project funded by the Overseas Development Administration (UK) to develop methods for bovine class II MHC typing based on characterization of genes that encode expressed class II products. Scientists at Roslin examined a number of typing techniques based on use of the polymerase chain reaction (PCR) to amplify defined stretches of DNA. Two complementary methods applicable to a range of class II genes were chosen. Types are assigned by analysis of restriction fragment length polymorphism (RFLP) in PCR-amplified segments of the class II gene; the presence or absence of a series of restriction enzyme sites is determined from the sizes of the restriction fragments. The PCR-RFLP assignments are then checked and confirmed by assessment of single-strand conformation polymorphism (SSCP), in which sequence-dependent variation in the migration of the denatured PCR products is used to distinguish different class II genes. Both the PCR-RFLP and SSCP methods for typing have been transferred to ILRAD, where they are being used to evaluate MHC-related effects on the efficacy of ILRAD's experimental vaccine when applied in field trials. Another important aspect of the project has been cloning and characterizing full length complementary DNA for a number of bovine class II genes. More specifically, the ILRAD-Roslin project has established, among many other facts, that class II products from both the DR and DQ loci are expressed by bovine immune cells.

All vaccine development research programs need some way of typing class II MHC molecules. The development of rapid DNA-based methods to define the number and variety of expressed bovine class II MHC genes will provide the basis for rigorous studies of antigen presentation by the products of these genes and an assessment of their consequences in the immune responses of cattle populations to improved vaccines.

The technologies developed in this collaborative research have provided an ideal opportunity to acquire enhanced knowledge of antigen presentation. This, in turn, will improve ILRAD's capacity to evolve improved antigen delivery strategies for the East Coast fever vaccine under development at the Laboratory.

This article is based on a report written by ILRAD scientist Declan McKeever. The scientists at the Roslin institute, in Edinburgh, who developed the improved MHC typing methods described are George Russell and Roger Spooner. This research is funded by the Overseas Development Administration of the UK.



This simplified diagram illustrates the steps by which bovine T lymphocyte cells recognize antigen.

Peptide molecules of degraded antigens are presented to T lymphocytes on the surface of antigen-presenting cells, such as a macrophage, in a binding cleft of a bovine MHC molecule. T cells recognize antigen only when it is associated in this way with a 'self' MHC molecule.

Types of MHC molecules vary among individual animals. ILRAD scientists need methods with which to characterize these MHC molecules to determine if this polymorphism will affect the efficacy of the novel p67-based vaccine against East Coast fever now under development at the Laboratory.

Ph.D. Theses

A *Trypanosoma congolense*-specific antigen released in the course of an infection is identified as a thiol protease precursor

Standardized reagents, including trypanosome antigens, are needed to support research in the epidemiology of trypanosomiasis. A peptide doublet of *Trypanosoma congolense* with a molecular weight of 38/40 kiloDaltons (kDa) and recognized by diagnostic monoclonal antibodies was used to raise polyclonal antibodies. One of these antibodies was used to screen a complementary DNA (cDNA) library from which 14 positive clones were identified. Antibody subpopulations selected by 10 of the 14 clones specifically recognized the 30/40-kDa polypeptides in lysates of different isolates of *T. congolense.* These recombinant antigen-selected antibody subpopulations appeared to have retained the species-specificity of the original polyclonal.

A clone with a cDNA insert of 1.6 kilobases, which had hybridized with all the other positive clones, was further characterized and sequenced. Results of a time-course digestion of *T.*

congolense DNA with restriction enzymes revealed that the gene encoding the *T. congolense* species-specific antigen occurs as an imperfect tandem repeat in the genomes of these parasites, with an estimated copy number of between 20 and 30.

The gene appears to be polymorphic among three isolates of *T. congolense.* A complete nucleotide sequence of the cDNA was obtained. Analysis of the whole of the deduced amino acid sequence revealed a number of domains identified as potential signal sequences. A homology search in databases revealed a high degree of identity of the deduced protein sequence to cysteine proteases from both animal and plant sources.

The gene is one of two studied that encode antigens secreted by trypanosomes or released by the parasites on dying into the blood and other tissues of mammalian hosts. Characterizing these antigens and making them available will offer scientists standardized reagents for use in studies of trypanosome epidemiology.

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Summary of a thesis abstract presented for a Ph.D. granted in 1993 by the Department of Biology and Biochemistry, Brunel University, UK.
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An extra chromosomal DNA molecule of *Theileria parva* encodes mitochondrial protein

Theileria parva, a protozoan parasite of cattle, contains an extra chromosomal DNA molecule with an apparent mobility of 7.1 kilobases in agarose gels. This molecule was characterized to determine whether it played a role in parasite virulence or, more importantly, in the unique ability of *T. parva* to 'transform' bovine lymphocytes. In addition, as an extra chromosomal element, it was potentially a good starting point for the construction of transfection vehicles.

A total of 5893 base pairs of this extra-chromosomal molecule have been fully sequenced and analysed. The molecule is linear in structure and contains inverted repeat sequences at its telomeres. The sequence shows that the DNA may code for apocytochrome b and polypeptide I and III of cytochrome c oxidase, protein components of the last two mitochondrial electron transport complexes. Apocytochrome b is of interest because it may be the target of hydroxynapthaquinones the class of drugs used in chemotherapy for East Coast fever.

The DNA molecule also contains several unique short stretches of discontinuous sequences that are similar to both large (LSU) and small (SSU) ribosomal subunit RNA of *Escherichia coli.* Five fragmented ribosomal RNA-like sequences, LSU1-LSU5, can be folded by inter-and intra-molecular base pairing into the phylogenetically conserved domains IV and V of the LSU ribosomal RNA. Other short stretches of sequence with similarity to SSU rRNA and other regions of LSU rRNA were tentatively identified. ,

The protein coding potential of the DNA molecule is characteristic of mitochondrial DNA and its structure and the presence of scrambled rDNA sequences is reminiscent of the mitochondrial DNA of *Chlamydomonas reinhardtii.* Other protozoan parasites in the same phylum as *Theileria,* such as *Plasmodium, Babesia, Eimeria* and *Toxoplasma,* contain related DNA molecules. These molecules are different in structure to the *T. parva* molecule but the conservation of the coding potential argues for a functional significance of this family of related DNA molecules.

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Summary of a thesis abstract for a Ph.D. awarded in 1993 by the Department of Medical Parasitology, London School of Hygiene and Tropical Medicine.
ILRAD Ph.D. supervisor: *Vish Nene*

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ILRAD was founded in 1973 to conduct research into better ways of controlling livestock diseases. The current primary goal of the Laboratory is to develop safe, sustainable and cost-effective methods of controlling the most important parasitic animal diseases in Africa and other developing regions: trypanosomiasis, transmitted to animals by tsetse flies, and tick-borne diseases, particularly East Coast fever. An international staff of about 50 scientists conducts basic research, much of it aimed at the development of vaccines, in bio-chemistry, cell biology, epidemiology, genetics, immunology, molecular biology, pathology, parasitology and the socioeconomics and environmental impacts of livestock disease control.

ILRAD is one of 18 international agricultural research centres sponsored by the Consultative Group on International Agricultural Research (CGIAR). The secretariat of the CGIAR is located in the World Bank headquarters, in Washington D C. The CGIAR is an informal umbrella organization of 40 national governments, international organizations and private foundations that together provide about US$230 million annually to the 18 centres for research, training and advisory services. The CGIAR aims to help farmers in developing countries increase their production of staple food crops, livestock, fish and trees in ways that improve the nutrition and well-being of low-income peoples and the management of natural resources.