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Vector-borne diseases occur in more than 100 countries and affect about half of the world’s population. They are both emerging and resurging, and consequently result in a high burden of disease that reflects inadequate impact of control measures. Effective prevention strategies can reverse this trend, and vector control is a key component of such strategies aiming at interrupting transmission.

Accordingly, in the context of TDR’s new vision and strategy, a strategic framework and implementation plan was developed for research into **Innovative vector control interventions** (Business Line 5) with the objective of developing and evaluating improved and innovative vector control methods for prevention of human African trypanosomiasis, malaria, dengue fever and Chagas disease.

BL5’s activities range from basic research in vector genomics to vector control tool development and testing in real-life situations. BL5’s operational approach, defined during a broad stakeholder and expert consultation meeting in April 2007, involves grants to dedicated networks of research institutions and control services in disease-endemic countries (DECs) as well as to research institutions in developed countries to address well-defined country needs through commissioned research. The approach of this BL is unique in that the research projects that form the focus of activities are being funded for long-term periods of three years, with the possibility of extension for another two years. Following the initial issuance of ten such long-term grants for multi-country studies in 2008, there will be no new grants approved until the current objectives are achieved.

The key stakeholders involved in BL5 activities are research institutes and control services worldwide, the International Glossina Genomics Initiative consortium, the Bill and Melinda Gates Foundation, the Foundation for the National Institutes of Health (NIH), and the World Health Organization’s (WHO) headquarters and regional offices. TDR convening power helped to bring the different stakeholders together in fostering joint efforts.

**Overview and highlights**

In the first year of the BLs implementation, the portfolio of 10 long-term multi-country grants was developed for targeted diseases (human African trypanosomiasis [HAT], malaria, dengue and Chagas disease), calls were issued and grants were finalized and approved. In addition, 80% of the Glossina genome sequencing was achieved by the International Glossina Genomics Initiative (IGGI), an initiative in which TDR is playing a major facilitating role; African investigators contributed significantly to the generation and exploitation of this genome data. In related capacity-development activities, the third annual short course in Glossina functional genomics was organized at the South African National Bioinformatics Institute (SANBI), University of the Western Cape, under TDR auspices. Additionally, the new TDR-supported African Regional Centre for Training in Biosafety for Human Health and the Environment at the University of Bamako organized its first biosafety training course in November 2008. A similar course is to be staged in 2009 at soon-to-be-opened regional biosafety training centres in Asia and Latin America.
In November 2008, the first TDR-supported course in laboratory biosafety and biosecurity was organized at the University of Bamako by the Biorisk Reduction for Dangerous Pathogens unit of WHO’s Department of Epidemic and Pandemic Alert and Response (EPR). This course involved participants from Asia and Latin America as well as from Africa. Such courses support the involvement of DECs in generation and exploitation of *Glossina* genome data as well as in future assessment of vector control methods using genetically modified disease vectors.

**Leverage and contributions to empowerment and stewardship**

BL5’s research work implemented by institutions and networks and its sponsorship of training courses make a major contribution to research stewardship and empowerment goals. Stewardship and empowerment goals also are furthered by the BLs work with DEC control services in Africa, Asia and the Americas to develop and field-test enhanced integrated vector control methods suitable for large-scale implementation. The fact that BL5’s research activities are conducted with direct involvement of the national disease control programs also enhances their sustainability by ensuring policy-maker commitment.

The BL also contributes to stewardship objectives through mobilization of the HAT community around the generation of *Glossina* genome sequence data and its exploitation for innovative vector control. Through the creation and support of the International *Glossina* Genomics Initiative (IGGI), TDR has leveraged significant donor support for the *Glossina* sequencing initiative. Similarly, work on genetically modified vectors has leveraged significant involvement from the Bill and Melinda Gates Foundation and the Foundation for NIH.

Overall, implementation of BL5’s work plan is on track despite some delays. For instance, seven of the funded multi-country grants for disease-specific research are on track to achieve their milestones. In the case of the other three such grants, there were delays in release of funds or project approvals, and implications of those delays will be reviewed during the third Strategic and Scientific Advisory Committee (SAC) meeting, 30 March–2 April 2009. Conversely, the very recent development of new genome sequencing technologies means that completion of the *Glossina* genome sequencing (using 454 FLX machines) is to be significantly accelerated, and is now due to be completed in 2009. Otherwise, no major changes are anticipated in the implementation plans of BL5 for 2009, although progress made and changes in the global research environment could potentially require further fine-tuning of activities.
1. Context, strategic objectives and framework

1.1. Context and rationale

Vector-borne diseases occur in more than 100 countries and affect about half of the world’s population. These diseases — transmitted by insect vectors or with the involvement of intermediate hosts or reservoir hosts — are among the most neglected tropical diseases. Disease prevalence and transmission is highly dynamic, with patterns of both new and resurgent vector-borne diseases resulting in a high burden of disease, estimated at about 56 million disability adjusted life years (DALYs). Effective prevention strategies can nonetheless reverse this trend, and vector control is a key component of such strategies, aiming to reduce or interrupt transmission. The need for new and improved vector control tools is particularly acute in the case of malaria, dengue, HAT and Chagas disease. Research can thus play an important role in design, development and testing of improved and innovative vector control tools and strategies. In this context, particular crosscutting needs and gaps have been defined, as well as needs and gaps for each priority disease in the BL5 research programme.

Disease-specific issues

HAT

A decline in vector control operations has hampered control of human African trypanosomiasis (HAT), particularly due to the inadequacy of drugs and other interventions. Vector control methods (e.g. traps, screens, application of insecticides on traps) to eliminate tsetse fly populations or at least reduce densities also have not demonstrated sustainability over time at the community level due to difficulties in using the tools and the variability in attractiveness of the traps to different species of tsetse flies. There is both a need and an opportunity to design new and improved tools and strategies in light of the nearly completed sequencing of the Glossina genome.

Malaria

In recent years, the contribution of vector control to the interruption of malaria transmission has been limited, due to still-deficient knowledge about vectors and their environments, to poor implementation of existing interventions on large scales, to the spread of vector resistance to insecticides and to limited resources. Consequently, there remains the need to develop new vector control methods and improve implementation of existing strategies. Research needs and opportunities include improvement of performance and field implementation of insecticide-treated materials, indoor residual spraying of insecticides, biological control of vectors, environmental management and future deployment of genetically modified vectors.

Dengue

The resurgence of dengue globally suggests that the current, admittedly limited, arsenal of control measures has not been effective or applied with sufficient rigour. In the absence of any effective drug treatment or vaccine, vector control remains the primary intervention for dengue prevention and control. Recent research has focused on the increased optimization of vector sampling methods, improvement of insecticide applications and development of a range of contextual community-based vector control interventions.

Chagas disease

In the 1990s, Chagas disease elimination campaigns, based on the application of insecticides to control domestic triatomine populations, achieved considerable success in the Americas, particularly in the Southern Cone region. However,
this approach has been ineffective against the invasion of triatomine bugs, particularly from peridomestic and sylvatic areas in the Andean region of Latin America as well as in Central America. As a result, the development of new and improved tools that are effective in those regions and of tools to prevent re-infestations of triatomine populations elsewhere are high priorities. Potential complementary control approaches include an integrated vector management programme that combines peridomestic environmental management and use of insecticide-treated materials.

Crosscutting research themes: genome sequencing and genetic modification

Across all diseases, there is a continuing need to initiate and facilitate insect vector genome sequencing and to exploit genome data with the involvement of DEC countries, investigators, institutions and public-private partnerships. This will provide opportunities for developing tools and generating knowledge useful for designing new vector control approaches. Furthermore, there is a need to build partnerships and strengthen the capabilities of DEC researchers and health workers to undertake vector research and control through enhanced transfer of new technologies to DECs.

There is also a need to explore new methods for disease vector control, building upon biotechnology advances as well as on successes in the control of agricultural pests. Research opportunities exist for improving biological and environmental control strategies as well as for development and deployment of genetically modified (GM) vectors. Over the past two decades, TDR and other partners have led an initiative for development of GM malaria and dengue vectors so as to interrupt pathogen transmission. Currently, the Bill and Melinda Gates Foundation’s Grand Challenges for Global Health (GCGH) initiative is the main funder of the research effort. TDR, meanwhile, is addressing requirements for potential field deployment of GM malaria and dengue vectors such as site selection and characterization; assessment of biosafety and efficacy; and ethical, legal and social implications (ELSI).

Changes in global context

The year 2008 saw a dynamic and changing global research environment. Key developments and events are described briefly below, with implications of changes in the global context for the BL5 strategic plan described in Section 3.

• The Roll Back Malaria (RBM) Partnership developed and launched a Global Malaria Action Plan (GMAP) in September 2008 to provide a global framework for action around which partners can coordinate their efforts to support countries.

• The Malaria Eradication Research Agenda Initiative (MalERA) began activities in November 2008 following public launch of GMAP.

• Field evaluation of genetic modification-based control methods for the interruption of dengue and malaria transmission appeared to be imminent following semi-field trials of genetically-modified *Aedes aegypti* mosquitoes in Malaysia (September–December 2007) as well as GCGH-sponsored research on GM vectors.

• WHO established a Global Partnership for Eliminating Chagas Disease (2007), which will be relevant to the development and evaluation of vector control tools and strategies by BL5.

• New technologies were developed for genome sequencing that have vastly reduced its cost and could significantly speed completion of the *Glossina* genome sequencing.
1.2. Strategic objectives

The overall goal of BL5 activities is to support the development and evaluation of improved and innovative vector control methods for the prevention of neglected diseases such as HAT, malaria, dengue and Chagas disease. This includes basic research into vector genomics and ecology as well as development of new and improved tools and testing in real-life situations. The BL contributes to the overall TDR aim of facilitating focused innovative research addressing country priority needs that are not adequately addressed by partners (TDR strategic objective 3). BL5’s activities contribute to TDR’s overall vision and strategy by promoting:
1) harmonization of global research efforts,
2) enhanced DEC health research leadership and
3) improved access to superior proven interventions.

The specific objectives of this research programme are to:

1. Promote the development and testing of new methods for improving HAT vector control and support the generation and exploitation of Glossina genome sequence data.
2. Advance the development and evaluation of new and improved integrated methods for malaria and dengue vector control.
3. Progress the development and evaluation of alternative methods to prevent re-infestation and control Chagas disease vectors.

Each objective has built-in research capacity-strengthening components.

1.3. Strategic framework and operational approach

BL5’s activities range from basic research in vector genomics to vector control tool development and testing in real-life situations. The strategic framework and operational approach (Fig. 1) was defined during a broad stakeholder and expert consultation meeting in April 2007. It involves grants to networks of investigators to address well-defined country needs through commissioned research. Networks are defined as research groups composed of at least three DECs, representative of different epidemiological and eco-climatic conditions and collaborating with non-endemic countries in multi-country research activities towards common goals. For each target disease, the research process includes several steps:

• Identification of critical gaps in disease vector control methods and strategies through knowledge review;
• Exploitation of current knowledge base and/or conduct of studies to generate new knowledge to fill the gaps identified;
• Development of improved vector control methods and strategies with large-scale implementation potential based on knowledge exploitation;
• Evaluation under field or semi-field conditions of improved methods and strategies developed and, if needed, application of further modification or improvement before final validation;
• Guidance provided for optimal large-scale implementation of the improved control methods and strategies;
• Recommendation for use of the interventions in disease control.

The approach of this BL is unique in that the disease research projects that are a large focus of activities are being funded for relatively long-term periods of three years, with the possibility of another two-year extension. Following the initial issuance of 10 such long-term grants to research networks for multi-country studies in 2008, there will be no new grants approved until the current objectives are achieved.
Administratively, there are four types of funded BL5 activities: 1) large, multi-country disease research grants; 2) capacity-building activities and training for biosafety; 3) SAC initiatives, particularly coordination of the International Glossina Genomics Initiative (IGGI) consortium for generation and exploitation of Glossina genome sequence data; 4) BL secretariat coordination of activities. The end-products and outcomes and their success indicators are described by objective in Table 1 and the framework for monitoring progress and milestones is described in Figs. 2-5.

BL5’s Strategic and Scientific Advisory Committee (SAC) is responsible for evaluating the research projects through annual meetings (see Annex 6.4 for details of SAC responsibilities and membership). The TDR secretariat for BL5 is responsible for coordinating the activities of the networks. Annual back-to-back meetings of the SAC and the networks’ principal investigators aid in overall coordination and evaluation. These meetings permit an active exchange of information and experience between researchers, SAC members and the TDR secretariat. Monitoring and evaluation also occur at the annual meetings of the IGGI consortium, research network coordination meetings and project coordination meetings, specifically for projects related to GM vector research. In addition, SAC members, the TDR secretariat and control staff from WHO HQ and regions follow up on the BL activities through site and expert visits. Finally, overall performance of this BL also is reviewed and evaluated through the internal TDR annual Portfolio Review and the annual session of TDR’s Scientific and Technical Advisory Committee (STAC).

Fig. 1. BL 5 strategic framework for innovative vector control interventions
### TABLE 1. BL 5 INDICATORS FOR END-PRODUCTS AND OUTCOMES

<table>
<thead>
<tr>
<th>BL objectives</th>
<th>End-products</th>
<th>Indicators for end-products</th>
<th>Expected outcomes</th>
<th>Indicators for expected outcomes</th>
</tr>
</thead>
</table>
| **Promoting HAT vector control**                  | Improved tsetse control methods and strategies developed and evaluated by 2012 | • Bait technology, odour-release systems and trapping materials developed and tested for improved traps and trapping methods for six tsetse species by 2011  
• Evidence based user-friendly decision support system for better planning and implementation of HAT vector control operations developed and tested in five African countries by 2012 | Promotion (through publications, meetings and media popularization) and adoption by countries by 2014 of the developed and tested HAT vector control methods and strategies and the guidance principles for their application | At least seven African countries endemic for HAT adopt the vector control methods and strategies by 2014 |
| **Glossina genome data**                          | Generated and made available for exploitation by 2011                        | • Tsetse genome sequencing completed, genome data made available to the public in accessible databases and published by 2011  
• 10–15 African investigators trained per year in bioinformatics, functional genomics and acquired experience in exploitation of genome data through networking by 2011 | Exploitation of *Glossina* genome data by DECs and worldwide investigators for innovative vector control strategies within 1–3 years after release of the genome sequence | Number of research projects funded about exploitation of genome data and number of publications that result from research activities about innovative tsetse control methods |
| **Advancing integrated malaria and dengue vector control** | Best practice guidance for deployment of GM vectors developed and evaluated by 2013 | • At least seven guidance principles documents generated and evaluated in six DECs and made available to the public by 2013  
• 15–20 DECs researchers/control staff trained in biosafety per year and per region for Africa, Asia and Latin America by 2011 | Application of the guidance principles by DECs for development of a framework for national assessment and approval of GM as a disease vector control tool by 2015 | At least fifteen DECs have developed national framework for assessment and approval of the use of GM vectors by 2015 |
<table>
<thead>
<tr>
<th>BL objectives</th>
<th>End-products</th>
<th>Indicators for end-products</th>
<th>Expected outcomes</th>
<th>Indicators for expected outcomes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Improved methods for packaging integrated malaria vector control approaches developed and evaluated by 2012</td>
<td>• Resistance of malaria vectors to insecticides and epidemiological impact of this assessed in six African countries by 2012 • Evidence-based approach for integrated malaria vector control suitable for large-scale implementation developed and evaluated in three African countries for improved planning and implementation of malaria vector control by 2012</td>
<td>Promotion (through publications, meetings and media popularization) and adoption by countries by 2014 of developed and tested malaria vector control methods and strategies and of the guidance principles for their application</td>
<td>At least fifteen countries endemic for malaria have adopted the vector control methods and strategies by 2014</td>
<td></td>
</tr>
<tr>
<td>Improved methods for targeted and integrated dengue vector control developed and evaluated by 2012</td>
<td>Optimal strategies for targeting source reduction and integrating approaches for suppression of dengue transmission developed and evaluated in two countries in Asia and two in Latin America for improved planning and implementation of dengue vector control by 2012</td>
<td>Promotion (through publications, meetings and media popularization) and adoption by countries by 2014 of the dengue vector control methods and strategies developed and tested and of the guidance principles for their application</td>
<td>At least six countries endemic for dengue have adopted the vector control methods and strategies by 2014</td>
<td></td>
</tr>
<tr>
<td><strong>Progressing Chagas disease vector control</strong></td>
<td>Methods for preventing reinfestation by triatomine bugs developed and evaluated by 2012</td>
<td>Morphological and molecular methods for identifying the origin and prevention of reinfestation by triatomine bugs developed and evaluated in four Latin American countries by 2012</td>
<td>Promotion (through publications, meetings and media popularization) and adoption by countries by 2015 of the Chagas disease vector control methods and strategies developed and tested and of the guidance principles for their application</td>
<td>At least ten countries endemic for Chagas disease have adopted the vector control methods and strategies by 2015</td>
</tr>
<tr>
<td>Strategies for complementary or alternative Chagas disease vector control measures developed and evaluated by 2013</td>
<td>Evidence-based approaches for improved combination of control methods in domestic, peridomestic and sylvatic situations developed and evaluated in four Latin American countries for improved planning and implementation of Chagas disease vector control by 2013</td>
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</table>
**Figure 3:** Framework for monitoring integrated methods for malaria vector control milestones

**Generic stage**

1. Knowledge review
   - Knowledge review

2. Targeted studies to fill critical knowledge gaps
   - Targeted studies to fill critical gaps

3. Initial design of intervention
   - New design/improvement of methods

4. Testing intervention under controlled conditions
   - Testing under controlled conditions

5. Final design of intervention
   - Modification/improvement of methods

6. Testing intervention in real-life setting
   - Final testing in real-life setting

7. Intervention recommended for disease control use
   - Recommended by WHO for control use

---

**Research stage**

- Well on track/ahead of plan
- Slightly behind plan but likely to get on track
- Significantly behind plan

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**Vector interventions research stage**

- Field evaluation of the improved methods and strategies
- Provide guidance for optimal large-scale implementation
- Testing in laboratory and/or semi-field
- Design evidence-based integrated intervention methods and strategies
- Malaria vector biology, ecology, resistance to insecticides, application of vector control methods, genetically modified vector (GMV) deployment issues
- Identification of critical gaps in tsetse control methods and strategies

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**BL5: Improving HAT vector control**

**BL5: Integrated methods for malaria vector control**

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**Fig. 2.** Framework for monitoring HAT vector control milestones
**Fig. 4.** Framework for monitoring dengue vector control milestones

**Fig. 5.** Framework for monitoring Chagas disease vector control milestones
2. Key stakeholders, roles and responsibilities

The stakeholders involved in the activities covered by BL5 are worldwide research and control institutions, the International Glossina Genomics Initiative consortium, the international research supporting/funding organizations and WHO departments and regions. Their specific activities, roles and responsibilities are described below.

**Research institutions and control services** are collaborating in the context of dedicated research networks established as part of the portfolio of 10 multi-country research projects. One outstanding example of such collaboration is the involvement of the Pan African Tsetse and Trypanosomiasis Elimination Campaign (PATTEC) country representatives in three HAT vector control research networks of African and developed-country research institutions. Similarly, national malaria, dengue and Chagas disease control programmes are involved in the networks addressing related disease-specific research issues. The research institutes and countries involved in the different BL5-funded projects on HAT, malaria, dengue and Chagas disease vectors are detailed in Annex 6.5.

The members of the International Glossina Genomics Initiative Consortium provide support to genome sequencing and data exploitation efforts as follows:

- **The Wellcome Trust Sanger Institute** is responsible for sequencing the *Glossina m. morsitans* genome (80% of genome sequencing was achieved in 2008) as well as contributing to other consortium activities.

- **The Institut de Recherche pour le Développement (IRD)** and French genome sequencing centre Genoscope are collaborating in sequencing of several thousand full-length cDNA of *Glossina p. gambiensis*.

- **The University of Tokyo** is collaborating in the sequencing of 100 000 bacterial artificial chromosomes (BAC) ends, 6 BAC clones, 10 000 cDNAs and tsetse symbionts *Wigglesworthia* and *Sodalis*.

- **Yale University School of Medicine, Liverpool School of Tropical Medicine, IRD, Institute of Tropical Medicine Antwerp (ITMA) and the South African National Bioinformatics Institute (SANBI)** have contributed to the generation and normalization of the expressed sequenced tags (ESTs) and bacterial artificial chromosomes (BAC) libraries, which are now being used to facilitate the sequencing processes.

- Other partners contributing to mobilization of research and control communities include the Kenyan Agricultural Research Institute (KARI), Tanzanian Trypanosomiasis Research Institute (TTRI), Ugandan National Livestock Research Institute (NaLIRI) and WHO Regional Office for Africa.

**The Bill and Melinda Gates Foundation (BMGF) and the Foundation for the National Institutes of Health (FNIH)**

In line with the April 2007 consultation meeting recommendations, stakeholder roles are defined to ensure complementary actions as follows: 1) BMGF and FNIH are funding the technical development of genetic control methods and eventual field testing through the Grand Challenges for Global Health (GCGH) initiative; 2) TDR is focusing on research and capacity-building to address requirements for potential field deployment of genetically modified malaria and dengue vectors. This includes research and capacity-building to provide best practice guidance for site selection and characterization, assessment of biosafety and efficacy and consideration of ethical, legal and social implications (ELSI) of eventual field trials.
In this context, TDR, WHO control departments and BMGF/FNIH are co-organizing and co-funding a series of technical and public consultations on genetically modified disease vectors, beginning with a technical consultation 4–6 May 2009. With respect to ELSI, TDR and the Ethical, Social and Cultural (ESC) working group of the GCGH are collaborating whereby TDR is developing good-practice guidance documents for potential field-testing of GM vectors, while ESC is funding research to examine strategies to overcome potential ELSI-related barriers to GM vector deployment.1

**WHO headquarters departments and regional offices**

WHO vector research and control staff participate as observers on BL5’s SAC. They also play a role in advising TDR-funded researchers and evaluating research activities through site visits and expert visits. Complementary to the activities of the newly-established TDR regional biosafety training centres in Africa, Asia and Latin America, BL5 also is supporting a three-year “train the trainers” programme for laboratory biosafety and biosecurity; this is being implemented by WHO’s Epidemic and Pandemic Alert and Response (EPR) biosafety and laboratory biosecurity unit. Additionally, a WHO vector control working group follows up on vector research and control activities across WHO departments and in TDR in monthly meetings.

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1 - The good practice guidance documents are being developed in conjunction with the Mumford project (ID No. A70551) and the activities of TDR regional biosafety training centres.
3. Implementation plan for 2008–2013 and progress

3.1. Plan, progress and key milestones

During the 2008 reporting period, BL5’s portfolio was developed and implemented, including finalization of ten multi-country research grants to networks to address key disease-specific research needs and creation of regional biosafety training centres in Asia, Africa and Latin America (Annex 6.5). Additionally, there was significant technical progress made in the Glossina sequencing activity, and a Glossina comparative genomics course for Africa was organized. Finally, the first regional biosafety training course for Africa and the first laboratory biosafety and biosecurity courses for Africa, Asia and Latin America were organized. Key highlights of progress are described below and summarized in Table 2 and Fig. 3.

1. Ten multi-country disease research networks were created, and research activities initiated, on dengue, Chagas, HAT, and malaria vector control.

The research networks involve research institutions in north and south as well as control services, and have been funded to conduct research on disease-specific objectives. Grants funded included: three to networks for HAT research (objective 1); five to networks for malaria and dengue research (objective 2); and two to networks for Chagas disease (objective 3). Each was funded with an annual budget ranging from US$ 150,000 to US$ 250,000. In terms of the approval process, the first BL5 SAC meeting (17–19 December 2007) reviewed initial proposals for the package of multi-year research grants. Following approval of seven of the ten grants, the first principal investigators’ meeting took place back-to-back with a second SAC meeting from 31 March to 4 April 2008, contributing to completion of the grants portfolio. Each set of activities may be funded for an initial three years, with the possibility of extension for another two years.

2. Three regional biosafety training centres in Africa, Asia, and Latin America were created.

These centres will address issues of biosafety for human health and the environment in relation to the potential use of genetically modified vectors. Each is to be funded for three years at the level of US$ 50,000 to train an average number of 15–20 participants per year and per centre. The African centre at the Faculty of Sciences and Technologies of the University of Bamako, Mali, began activities in 2008, with centres in Asia (India) and Latin America (Colombia) scheduled to begin operations in 2009.

3. The Glossina genome sequencing reached the 80% milestone, and is due to be complete in 2009 (see Annex 6.2.)

The sixth IGGI coordination meeting was organized from 22–24 November 2008 in Mombasa, Kenya, where the consortium announced the achievement of 80% of Glossina morsitans genome sequencing. The consortium has also developed an implementation plan to complete the sequencing in 2009 using a new, more efficient and significantly less expensive sequencing technique (section 5.2, Annex 6.2). Genome sequence assembly would follow in the same year and further annotation would be undertaken in 2010.

4. The third Glossina functional genomics course for Africa was organized and is being expanded into a network for functional genomics

This Glossina functional genomics course was organized by the South African National Bioinformatics Institute (SANBI) 4–8 August 2008 at the University of the Western Cape, South Africa. Eighteen
researchers from ten African countries attended the workshop. This activity will be expanded in 2009 into a network that will become an integral part of the IGGI consortium. Additionally, Glossina transcriptome data generated through training workshops has been transferred to the GeneDB database at the Sanger Institute to enhance public access.

5. The first regional biosafety training course for Africa and the first laboratory biosafety and biosecurity course for Africa, Asia and Latin America were organized.

- The first training course in biosafety for human health and the environment for Africa was organized 17–28 November 2008 in Bamako, Mali, by the Regional Biosafety Training Centre created at the University of Bamako’s Faculty of Sciences and Technologies as part of the BL5 grant portfolio. About 20 participants from 11 African countries attended the course. A similar course is to be staged in 2009 at soon-to-be-opened regional centres in Asia and Latin America.

- Back to back, the first global course in Laboratory biosafety and biosecurity was also launched in Bamako (3–7 December 2008). This TDR-funded course was organized by WHO/EPR, it involved eleven participants from seven countries (three from Asia, six from Africa and two from Latin America).

- A coordination meeting of GM-related BL5 projects was organized from 29 November–2 December 2008 in Bamako, Mali. The meeting harmonized the course content and operational procedures for the regional biosafety training centres being established in Africa, Asia and Latin America. It also established mechanisms for testing and disseminating best practice guidance on the use of GM vectors.
### Table 2. Implementation Plans and Progress of 2008–2013 Activities

<table>
<thead>
<tr>
<th>BL objectives</th>
<th>Activities (2008–2013)</th>
<th>Milestones and target dates</th>
<th>Progress made</th>
<th>Revised dates</th>
</tr>
</thead>
</table>
| 1. Promoting HAT vector control | 1.1 • Development and testing of improved traps and trapping methods  
  • New and improved evidence-based approach for HAT vector control operations  
  • Trapping materials and bait technology improved by 2009;  
  • Odour release systems developed and evaluated by 2010;  
  • Improved trapping system evaluated by 2011  
  • Knowledge gathered and published for filling gaps in HAT vector control methods and tsetse population ecology, genetics and dispersal by 2009;  
  • Improved methods developed from knowledge exploitation for large-scale tsetse control by 2011  
  • Improved HAT control methods field evaluated and guidance provided for their implementation by 2012 | • On track with project A70594                                                                 | As the delay is likely to be recovered in 2009, milestone dates do not need revision                                                                 |                                                                               |
|               | 1.2 • Generation of *Glossina* genome sequence data  
  • Training DEC investigators in bioinformatics and functional genomics applied to *Glossina*  
  • *Glossina* genome sequencing completed by 2009  
  • *Glossina* genome sequence annotated by 2010  
  • *Glossina* genome sequence published by 2011  
  • 10-15 DEC investigators trained per year in bioinformatics and functional genomics activities by 2009  
  • DEC investigators undertaking bioinformatics and functional genomics activities by 2011 | • On track with project A70598 for DSS  
  • About four months’ delay for project A80132 | On track                                                                                                                                                                                                                   |                                                                               |
<table>
<thead>
<tr>
<th>BL objectives</th>
<th>Activities (2008–2013)</th>
<th>Milestones and target dates</th>
<th>Progress made</th>
<th>Revised dates</th>
</tr>
</thead>
<tbody>
<tr>
<td>2. Advancing integrated malaria and dengue vector control</td>
<td>2.1. • Development of best practice guidance principles for the use of GM vectors • Building capacity in DECs for assessment and management of biosafety for humans and the environment, and set up and management of regulatory principles and bodies</td>
<td>• Potential release sites for GM malaria and dengue vectors identified and characterized by 2009 • ELSI considerations addressed by 2011 • Criteria and guidance for field efficacy and safety evaluation of GM malaria and dengue vectors established and applied by 2013 • 15-20 researchers, staff in control services and decision-makers in DECs trained per year and per centre in assessment and management of biosafety for humans and the environment by 2009 • 15-20 DECs human resources trained in set up and management of regulatory bodies by 2011</td>
<td>• On track with project A70551 • On track for Africa but delayed by six months for Asia and Latin America</td>
<td>Delay could be reduced by organizing courses in 2009 in Asia and Latin America</td>
</tr>
<tr>
<td></td>
<td>• Knowledge gathered and published about malaria vector control methods and population biology, behaviour, ecology and genetics by 2009 • Improved methods developed from knowledge exploitation for integrated malaria vector control approaches by 2010 • New improved integrated malaria vector control methods evaluated and guidance provided for their implementation by 2012</td>
<td>• Malaria vector resistance to insecticides determined by 2009 • Epidemiological impact of vector resistance assessed by 2011 • Malaria vector resistance mechanisms to insecticides characterized by 2012</td>
<td>• Delayed by about six months • On track with project A70558 for four countries out of five</td>
<td>• Revision of date would be determined during the SAC and PI’s meeting in April 2009 • The fifth country will start in early 2009. Revision is not needed at this stage</td>
</tr>
<tr>
<td></td>
<td>• Development of optimal strategies for targeted and integrated dengue vector control in Asia and Latin America</td>
<td>• Knowledge gathered, published and disseminated by 2009 about existing gaps in dengue vector control methods and Aedes population biology, genetics and dynamics • Improved methods developed from knowledge exploitation for targeted and integrated dengue vector source reduction and transmission suppression by 2010 • New, improved targeted and integrated dengue vector control methods evaluated and guidance provided for their implementation by 2012</td>
<td></td>
<td>On track for one country out of four; the three countries delayed are expected to be back on track within four months</td>
</tr>
</tbody>
</table>
### BL objectives

#### 3. Progressing Chagas disease vector control

<table>
<thead>
<tr>
<th>Activities (2008–2013)</th>
<th>Milestones and target dates</th>
<th>Progress made</th>
<th>Revised dates</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>3.1</strong>&lt;br&gt;• Development and evaluation of improved methods for preventing re-infestation by triatomine bugs</td>
<td>• Molecular markers developed and used for Chagas disease vectors population biology studies by 2009  &lt;br&gt;• Knowledge gathered and published for filling gaps in Chagas disease vector control methods and population dynamics and dispersal and used to develop methods to assess the origin of re-infestation by 2011  &lt;br&gt;• Improved methods developed from knowledge exploitation and evaluated for the prevention of re-infestation by Chagas disease vectors by 2012</td>
<td>On track with project A70596</td>
<td></td>
</tr>
<tr>
<td><strong>3.2</strong>&lt;br&gt;• Development of alternative control methods for Chagas disease vectors</td>
<td>• Current sampling and control tools re-evaluated through knowledge generation for further improvement by 2009  &lt;br&gt;• New improved tools for Chagas disease vector control developed by 2011  &lt;br&gt;• New developed control methods evaluated for field efficacy and safety and guidance provided for their implementation by 2013</td>
<td>Delayed by six months</td>
<td>• Revision of date determined during the SAC and PIs meeting in April 2009</td>
</tr>
</tbody>
</table>
### Preparatory phase

Consultation to define priority research areas of work and *modus operandi* of networks

Advisory Committee meeting for selection of networks

### 1. Promote HAT vector control

1.1. Improving large-scale control of tsetse flies

- Improved traps and trapping methods

- New improved evidence-based approach for HAT vector control operations

1.2. Facilitating generation and exploitation of *Glossina* sequence data

- Tsetse genome sequence data generated

- DEC investigators trained in functional genomics

### 2. Advance malaria and dengue vector control

2.1. Addressing the requirements for deployment of G&C control methods

- Best practice guidance principles defined

- DEC research/control staff trained in biosafety and in set-up and management of regulatory bodies

2.2. Improving methods for integrated malaria vector control

- Resistance to insecticides and epidemiological impact assessed

- Evidence-based approach developed for integrated vector control

2.3. Improving methods for targeted dengue vector control

- Optimal strategies developed for targeted and integrated dengue vector control in Asia

- Optimal strategies developed for targeted and integrated dengue vector control in Latin America

### 3. Progressing Chagas disease vector control

3.1. Developing improved methods for preventing re-infestation by triatomine bugs

3.2. Developing new alternative control methods for Chagas disease vectors

### Follow-up and evaluation of activities

Advisory Committee and networks meetings

Site visits/experts’ visits

Annual review of the implementation of the business line activities

Fig. 6. Progress of BLS activities and milestones
3.2. Implications of progress/delays and global context changes on 2008–2013 plan

Delays in release of funds for approved projects and in selection of new proposals

There was a delay of about four months in the release of funds for one dengue project and one HAT project due to the introduction of a new Global Management System in WHO as well as because of ethical review-related issues. These delays can likely be overcome in 2009 in the project implementation phase. Approval of regional biosafety training centres in Asia and Latin America was also delayed due to the difficulties in obtaining viable proposals and the need to reissue calls repeatedly. However, the grants have now been awarded and these centres are scheduled to begin operations in 2009. To compensate for the loss of a course cycle in 2008, each centre will organize two courses in the coming year: one in April and a second in November.

The most serious delay experienced related to difficulties in obtaining viable grant proposals for two more disease research projects, one in malaria and another in Chagas disease. While these grants also have now been awarded, the delay has broader implications insofar as it leads to an asynchronous implementation of the work plan. The issue was discussed during the SAC/PIs meeting in April 2009 to explore adequate solutions.

Implication of changes in global context

The business plan falls well in line with the current global environment, and currently no major changes are anticipated. However, it remains important that in ongoing research for new vector control tools and approaches, BL5 continuously strives to address the objectives of the Global Malaria Action Plan (GMAP) to support global malaria control and elimination efforts. Other global context changes and issues that need to be considered are listed below.

- There is a need to expedite the process of helping DECs develop frameworks for assessment and approval of GM vectors as disease control tools. This requires accelerated development and testing of best practice guidance for use of GM vectors, capacity-building for biosafety assessment in DECs and engagement of WHO and partners in providing assistance at country level.

- New technologies have been developed for genome sequencing that have greatly diminished the cost of sequencing and can significantly accelerate the process of completing the Glossina genome sequencing. Consequently, TDR’s own plans in collaboration with the IGGI consortium are being fine-tuned to account for this expedited timetable.

- There is an ongoing need to continually harmonize and coordinate the TDR research for the prevention of HAT, malaria, dengue and Chagas disease with WHO control departments such as NTD, GMP and EPR.
3.3. Specific activities planned for 2009

In the first two quarters of 2009, the following activities are planned:

- PIs meeting, 30–31 March 2009, Buenos Aires, Argentina. Agenda to include progress report, information exchange and interaction with SAC members.
- SAC meeting 01–02 April 2009, Buenos Aires, Argentina. Agenda to include review of progress report and grant renewal requests; strategic review of the work plan and SAC committee initiatives and recommendations.
- First round of regional training courses in Biosafety for human health and environment in Asia and Latin America, April 2009, Centre for Research in Medical Entomology, Madurai, India, and University of Antioquia, Medellin, Colombia.
- First Technical Consultation on GM vectors, 04–06 May 2009 (WHO/HQ) co-organized by WHO/TDR and BMGF/FNIH, to be followed by a public consultation at a later date to be determined.

In the second two quarters of 2009, the following activities are planned:

- Coordination and follow-up on the implementation of the 10 long-term disease-specific research grants (e.g. site visits, expert visits).
- Second round of regional training courses in Biosafety for human health and the environment for Africa, Asia and Latin America; also, in Madurai, India, a back-to-back global coordination meeting of PIs of all GM-related projects, October/November 2009.
- Second annual Global laboratory biosafety and biosecurity course for Africa, Asia and Latin America in Madurai, India (December 2009).
- Portfolio review and development of next biennium budget (12–16 October 2009).
- Seventh International Glossina Genomics Initiative consortium meeting (December 2009).
4. BL leverage, contributions to empowerment and stewardship, and synergies with other TDR business lines

4.1. Leverage

TDR’s initiative in 2004 that led to the formation of the International Glossina Genomics Initiative (IGGI) consortium has generated enormous support for genomic sequencing of HAT disease vectors and exploitation of the genome data. This is an outstanding example of how TDR investment on a modest scale has leveraged significant additional support for a research activity. With respect to genetically modified vectors, TDR activities also have leveraged significant donor interest and support. Most recently, this is reflected in the joint sponsorship by BMGF and the FNIH of the technical consultation on genetically modified vectors, co-organized with TDR and WHO control departments on 4–6 May 2009 (WHO HQ). The details of the key donors and funding available to these two activities are described in Table 3.

### TABLE 3. IGGI CONSORTIUM SUPPORT FOR GENOMIC SEQUENCING AND OTHER SUPPORT FOR GM VECTOR COLLABORATIONS

<table>
<thead>
<tr>
<th>Organization</th>
<th>Activities</th>
<th>Approximate contribution (US$)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wellcome Trust Sanger Institute</td>
<td><em>Glossina morsitans</em> genome sequencing for 3x</td>
<td>3 000 000</td>
</tr>
<tr>
<td>Yale University</td>
<td>Generation of cDNA from various <em>G. m. morsitans</em> tissues and BAC libraries</td>
<td>15 000</td>
</tr>
<tr>
<td>Liverpool School of Tropical Medicine</td>
<td>Generation of cDNA from various <em>G. m. morsitans</em> tissues</td>
<td>15 000</td>
</tr>
<tr>
<td>IRD/Genoscope</td>
<td>Generation of cDNA from various <em>G. palpalis gambiensis</em> tissues and sequencing of full-length cDNA</td>
<td>30 000</td>
</tr>
<tr>
<td>University of Tokyo</td>
<td>Sequencing of full-length <em>G. m. morsitans</em> cDNA</td>
<td>15 000</td>
</tr>
<tr>
<td>BMGF/FNIH</td>
<td>Production and publication of GM vectors cage containment guidance document</td>
<td>20 000</td>
</tr>
</tbody>
</table>
4.2. Contribution to overall empowerment and stewardship objectives

BL5 activities contribute to overall TDR empowerment objectives by supporting:

(i) Exploitation of *Glossina* genome sequence data through training in bioinformatics and functional genomics;

(ii) Training in assessment and management of biosafety for human health and the environment, as well as support towards establishment and management of regulatory bodies for ethical and biosafety reviews in preparation for deployment of genetically-modified vectors;

(iii) Training of DEC country researchers (e.g. doctoral and master’s degree students) in the context of large multicountry-funded research projects.

BL5 facilitation of the International *Glossina* Genomics Initiative (IGGI) consortium contributes to overall TDR stewardship objectives, bringing stakeholders together to review and take action on research needs and priorities. In addition, through IGGI activities BL5 has greatly contributed to mobilizing and engaging the HAT research community globally, which had until the development of the IGGI initiative become almost a “neglected community” due to reduced donor interest and support.

4.3. Elements enhancing sustainability of BL5 outcomes

The operational and organizational framework used for the research and development of vector control tools enhances the potential sustainability of BL5 outcomes. The early involvement of potential users of products in overall planning and better interactions between research and control facilitate a smoother transition from research to implementation, improving uptake of new methods and strategies by countries. Of particular importance to this BL are the involvement and buy-in of disease and vector control services in the R&D process and their subsequent involvement in developing guidance principles for large-scale use of strategies as well as training of end-users. The key BL components enhancing sustainability are:

**Framework for development of vector control tools**

As noted in section 1.3, the initial April 2007 consultation on BL activities involved country-level stakeholders from the beginning in the definition of needs and target objectives for planned research. Participants in this consultation included researchers and staff of national disease control services, decision-makers and international organizations supporting research activities.

**Involvement of control services with research institutes in the R&D process**

As indicated in section 2 and Annex 6.5, all BL5 research networks involve direct collaborations between research institutes and control services.

**Development of guidance principle for large-scale use of strategies; training of end-users**

In addition, country control services participate with researchers in developing guidance principles based on research findings and in related training activities that test these principles in action. For example, in the case of GM disease vector research, staff from control services and even decision-makers are participating in regional biosafety courses initiated by TDR.
4.4. Synergies with work of TDR business lines

The synergies with other BLs are presented in Table 4.

**TABLE 4. BL5 SYNERGIES WITH WORK OF TDR BUSINESS LINES**

<table>
<thead>
<tr>
<th>Interface with other BLs</th>
<th>Shared/complementary objectives</th>
<th>Related specific activities</th>
<th>Mechanisms for coherence and coordination</th>
</tr>
</thead>
<tbody>
<tr>
<td>BL1</td>
<td>Developing partnerships and mobilizing stakeholders</td>
<td>Facilitation of IGGI consortium activities, support to PATTEC operations</td>
<td>Communication and interaction</td>
</tr>
<tr>
<td>BL2</td>
<td>Building capacity in DECs and networking</td>
<td>Research and training</td>
<td>Communication and interaction</td>
</tr>
<tr>
<td>BL3</td>
<td>Developing innovative methods for disease control</td>
<td>Promoting exploitation of genomic data for disease control</td>
<td>Communication and interaction</td>
</tr>
<tr>
<td>BL9, BL11</td>
<td>Development of integrated control strategies</td>
<td>Malaria integrated control strategies</td>
<td>Communication and interaction</td>
</tr>
<tr>
<td>BLs 3–11</td>
<td>Contribution to access to superior interventions</td>
<td>Development and evaluation of control methods and strategies</td>
<td>Communication and interaction</td>
</tr>
</tbody>
</table>
5. Critical issues and suggested solutions

5.1. Implementation delays

As noted in section 3.2, difficulties in obtaining viable grant proposals for two disease research projects, (malaria and Chagas disease) resulted in significant delays in the implementation schedule. Implications for the overall implementation of the business plan are to be discussed during the next SAC/PIs meeting in April 2009.

5.2. Proposal for completion of Glossina genome sequencing project

By the end of 2008, the Wellcome Trust Sanger Institute had achieved 3x coverage of the *Glossina morsitans* genome sequencing, which effectively means that 80% of the tsetse fly genome has now been sequenced. However this still fell short of the IGGI consortium’s goal of achieving 10x coverage – which would not only complete the sequencing but also facilitate accurate genome sequence assembly, e.g. reconstruction of the DNA sequences thus obtained.

Meanwhile, new and less expensive technologies that have revolutionized DNA sequencing now appear able to make up for what had been a serious shortfall in donor financial support for the sequencing effort. Notably, a new 454 technology being increasingly used for sequencing activities is many times less expensive than conventional strategies. The output of the recently available 454 FLX machines with the titanium (tm) upgrade is up to 400 Mb per run. Thus, 12–15 runs should give close to 5 Gb of data. It is estimated that this new technology could be used to sequence *Glossina* much faster, and for a cost of only US$ 250 000. As a result, the IGGI consortium believes that the goal of reaching 10x coverage is not only realistic but can even be met on an accelerated timetable (estimated by end 2009). Therefore, the consortium is exploring sources of funding to harness this new technology and complete the 10x *Glossina* genome sequencing (Annex 2).

---

1 - (i.e. each nucleotide represented in 3 sequences)
6. Annexes

6.1. List of publications resulting from BL5 or related activities

Publications resulting from Molecular Entomology (BCV) final reports:


6.2. Proposal for completion of \textit{Glossina} genome sequencing by the IGGI consortium

A significant set of molecular resources is now available for \textit{Glossina}. This is largely attributable to the efforts of WHO/TDR that have allowed the small \textit{Glossina} community to gather under the umbrella of International \textit{Glossina} Genomics Initiative (IGGI) since 2004. The IGGI consortium has enabled various community-wide efforts to recruit funding sources to conduct several gene discovery projects.

The already completed resources include the analysis of three large tissue-specific EST libraries (midgut, fat body and salivary glands), smaller organ-specific EST projects (developmental stage-specific) and full-length cDNAs. We also have a BAC library available for the community use and have sequenced 50 000 BAC-ends that will be vital for genome assembly. IGGI has conducted several community annotations on the available ESTs, which have already been of great value to functional studies for community members.

Towards the genome sequence, we have been able to secure a grant from Wellcome Trust for limited sequencing at the Sanger Center. To date we have produced 2 447 308 reads, of which 2 127 617 have assembled. This is quite a high proportion, suggesting that the genome is nowhere near as complex or repetitive as some of the recent mosquito or worm genomes.
At the present time, the assembly includes:

**Contigs:**
- Total length: 345,988,465
- Number: 85,764
- N50: 6518
- Mean length: 4038
- Longest: 53,084

**Supercontigs:**
- Total length: 377,091,792
- Number: 25,760
- N50: 52,075
- Mean length: 14,639
- Longest: 1,053,091

In summary, the genome appears to be smaller than expected, and more than half of it is represented in scaffolds greater than 50 kb. This is extremely promising.

Recent technological advances have revolutionized DNA sequencing efforts. The traditional Sanger Sequencing methodology is no longer the technology of choice for many of the recently undertaken genome projects. Rather, 454 technology is being increasingly used for sequencing efforts. The cost of this technology is manyfold less that of traditional strategies. The output of the recently available 454 FLX machines with the titanium (tm) upgrade is up to 400 mb per run. Thus, 12–15 runs should give close to 5 gb of data. Given that we are starting from draft coverage due our existing sequencing data, we propose to do a 10x coverage. We would run this as a 50:50 mixture of shotgun and 3 kb paired end libraries for 14 runs, and do 600k+ reads from a 20 kb paired end library.

The cost of 15 runs is currently about US$ 100,000. To make sure that the data are assembled and genes predicted, we propose to build in a further 2FTE staff (~US$ 150k), one at Sanger and one at the European Bioinformatics Institute (EBI) in VectorBase. We are confident that having two designated annotators for one year would bring this project up to date. Therefore, the total cost to complete the Glossina genome sequence using the new technology would be US$ 250,000.

We are appreciative of the solid support that WHO/TDR has provided for this most neglected disease. We are confident that the completion of the WGS would advance this research field and lead to discoveries unique to tsetse physiology, including reproduction, olfaction and immunity. These areas are actively being researched in other disease vectors. Much of this knowledge has the potential to update our existing control methods and bring about new disease control strategies.

The timeline for completion of this project is depicted in Fig. 7.
6.3. Responses to specific JCB, standing committee and STAC requests

Limit research projects to outside with independent reviewing after 2–3 years

To ensure a fair review, renewal of funding and extension of part of a network project beyond three years would depend upon successful report with renewal request, following an in-depth review after 2–3 years by SAC, with an additional external review as proposed by STAC 30.

Involve potential users of products in overall planning to eventually achieve a smoother transition from research to implementation.

As already indicated under key stakeholders (section 2) and in Annex 6.5, all the BL5 research networks about vector control activities involve direct collaboration between research institutes and control services. In particular, the representatives of the Pan African Tsetse and Trypanosomiasis Elimination Campaign (PATTEC) are involved in all HAT vector control projects. In a similar manner, national malaria, dengue and Chagas disease control programmes are also involved in the research projects. For the guidance principles being developed for the potential use of genetically modified disease vectors, a link has been established with regional biosafety course coordinators and trainees involving researchers, staff from control services and decision-makers. In this way, they would help in the testing of the guidance principles. In addition, the guidance principles would be tested, validated and disseminated, and staff in national disease control services would be trained in their use. This would ensure better interactions between research and disease control services and would facilitate uptake of the research findings.

Define deliverables by describing potential impact: Fig. 1 and Table 1 provide a graphical illustration and description of the end-products and expected outcomes and their success indicators by BL5 objective and impact.

6.4. SAC responsibilities and membership

The BL5 SAC is responsible for evaluating research projects through annual meetings. Progress made in the three-year funded grants is evaluated each year, with renewal dependent upon a satisfactory report. Grants may be renewed for an additional two years beyond that, pending a positive in-depth review by SAC as well as external review (Annex 6.3).

In addition to providing a strategic direction for the BL, the SAC also advises the investigators on their work. The staff of WHO HQ and regions in charge of vector research and control participate in the SAC annual meetings as observers. This ensures that TDR vector research activities are understood by the different components of WHO and that their needs and concerns are fully reflected in the TDR activities.

MEMBERS
1. Dr Serap AKSOY (Chair), Yale University School of Medicine, Department of Epidemiology and Public Health, New Haven, CT, USA
2. Dr Roberto Barrera, Dengue Branch, DVBID, Centers for Disease Control and Prevention, San Juan, Puerto Rico
3. Dr Maureen COETZEE, Vector Control Reference Unit, National Institute for Communicable Diseases, Johannesburg, South Africa
4. Dr Aditya P. DASH, National Institute of Malaria Research, Delhi, India
5. Dr Liléia DIOTAIUTI, Laboratory of Triatomines and Epidemiology of Chagas Disease, Centro de Pesquisas René Rachou/FIOCRUZ, Belo Horizonte, Brazil
6. Dr Felipe GUHL, Centro de Investigaciones en Microbiologia y Parrasitologia Tropical (CIMPAT), Bogota, Colombia
7. Dr Pattamaporn KITTAYAPONG, Centre for Vectors and Vector-Borne Diseases, Faculty of Science, University of Mahidol, Bangkok, Thailand
8. Dr Michael J. LEHANE, Liverpool School of Tropical Medicine, Liverpool, United Kingdom
9. **Dr Atway MSANGI**, Tsetse and Trypanosomiasis Research Institute (TTRI), Tanga, United Republic of Tanzania

10. **Dr Hilary RANSON**, Liverpool School of Tropical Medicine, Vector Group, Liverpool, United Kingdom

11. **Dr Frédéric SIMARD**, Institut de Recherche pour le Développement (IRD), Bobo Dioulasso, Burkina Faso

12. **Dr Larry ZWIEBEL**, Department of Biological Sciences, Vanderbilt University, Nashville, TN, USA

**OBSERVERS**

This group includes representatives from research and control departments of WHO HQ (GMP, NTD, Public Health and Environment (PHE), EPR and TDR) and WHO regional offices.

6.5. **BL5-funded projects and SAC initiatives**

BL5-funded projects and SAC initiatives are described in Table 5.
## Table 5. BL5 Funded Projects and SAC Initiatives

<table>
<thead>
<tr>
<th>Project Identification</th>
<th>Principal Investigator</th>
<th>Institution</th>
<th>Project Title</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Objective 1: Promoting HAT vector control</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A70594</td>
<td>Patrick Guerin</td>
<td>University of Neuchatel, Institute of Biology, Switzerland</td>
<td>Development of trapping and target devices for controlling vectors of human African trypanosomiasis (HAT)</td>
</tr>
<tr>
<td>A70598</td>
<td>Stephen Torr</td>
<td>Natural Resources Institute, University of Greenwich at Medway, UK</td>
<td>A user-friendly decision support system to improve vector control operations against HAT</td>
</tr>
<tr>
<td>A80132</td>
<td>Johnson Ouma</td>
<td>Kenya Agricultural Research Institute/ Trypanosomiasis Research Centre, Kikuyu, Kenya</td>
<td>Integrated tsetse fly ecology and genetics for improved HAT control</td>
</tr>
<tr>
<td>A80210</td>
<td>Alan Christoffels</td>
<td>South African National Bioinformatics, University of the Western Cape, South Africa</td>
<td>Training course on <em>Glossina</em> functional genomics</td>
</tr>
<tr>
<td>A80032</td>
<td>Mathiew Berriman</td>
<td>Sanger Institute, Cambridge, UK</td>
<td>Development of web–based resources for handling and management of <em>Glossina</em> genome data</td>
</tr>
<tr>
<td>A80406</td>
<td>Junichi Watanabe</td>
<td>University of Tokyo, Japan</td>
<td>Generation and sequencing of additional <em>Glossina morsitans</em> full-length cDNA</td>
</tr>
<tr>
<td><strong>Objective 2: Advancing integrated malaria and dengue vector control</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A70551</td>
<td>John David Mumford</td>
<td>Imperial College London, UK</td>
<td>Best-practice guidance for deployment of genetic control methods against mosquito vectors in disease-endemic countries</td>
</tr>
<tr>
<td>A80130</td>
<td>Madama Bouaré</td>
<td>University of Bamako, Faculty of Science and Techniques, MALI</td>
<td>A biosafety training course in Mali for Africa related to potential release of genetically modified disease vectors</td>
</tr>
<tr>
<td>A80309</td>
<td>Tyagi Brij Kishore</td>
<td>Centre for Research in Medical Entomology, Madurai, India</td>
<td>Asian centre for training in biosafety assessment for human health and environment using genetically modified vector</td>
</tr>
<tr>
<td>A80310</td>
<td>Ivan Dario Velez</td>
<td>PECET-Program for the Study and Control of Tropical Diseases, Medellin, Colombia</td>
<td>Latin American training centre for biosafety of genetically modified vectors</td>
</tr>
<tr>
<td>Funding in US$</td>
<td>Disease</td>
<td>Countries involved</td>
<td>Research area</td>
</tr>
<tr>
<td>--------------</td>
<td>--------------------------</td>
<td>-------------------------------------------------------------------------------------</td>
<td>------------------------</td>
</tr>
<tr>
<td>240 000</td>
<td>Human African trypanosomiasis</td>
<td>Angola, Burkina Faso, Cameroon, Canada, Côte-d’Ivoire, Democratic Republic of Congo, Hungary, Italy, Kenya, Sudan, Switzerland and Tanzania</td>
<td>Vector control</td>
</tr>
<tr>
<td>199 784</td>
<td>Human African trypanosomiasis</td>
<td>Burkina Faso, Côte-d’Ivoire, Malawi, Tanzania, United Kingdom and Zimbabwe</td>
<td>Vector control, implementation research</td>
</tr>
<tr>
<td>200 000</td>
<td>Human African trypanosomiasis</td>
<td>Italy, Kenya, Tanzania, Uganda, United Kingdom and United States of America (USA)</td>
<td>Vector entomology, capacity strengthening</td>
</tr>
<tr>
<td>50 000</td>
<td>Human African trypanosomiasis</td>
<td>African countries, UK</td>
<td>Vector entomology, capacity strengthening, biotechnology and innovation</td>
</tr>
<tr>
<td>50 000</td>
<td>Human African trypanosomiasis</td>
<td>UK, HAT community worldwide</td>
<td>Biotechnology and innovation</td>
</tr>
<tr>
<td>20 000</td>
<td>Human African trypanosomiasis</td>
<td>Japan, HAT community worldwide</td>
<td>Biotechnology and innovation</td>
</tr>
<tr>
<td>186 880</td>
<td>Malaria and dengue</td>
<td>Brazil, India, Kenya, Mexico, Panama, Thailand and United Kingdom</td>
<td>Vector entomology, capacity strengthening</td>
</tr>
<tr>
<td>50 000</td>
<td>Malaria and dengue</td>
<td>African countries</td>
<td>Capacity strengthening</td>
</tr>
<tr>
<td>50 000</td>
<td>Malaria and dengue</td>
<td>Asian countries</td>
<td>Capacity strengthening</td>
</tr>
<tr>
<td>50 000</td>
<td>Malaria and dengue</td>
<td>Latin American countries, USA</td>
<td>Capacity strengthening</td>
</tr>
<tr>
<td>Identification</td>
<td>Principal investigator</td>
<td>Institution</td>
<td>Project title</td>
</tr>
<tr>
<td>----------------</td>
<td>------------------------</td>
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</tr>
<tr>
<td>A80371</td>
<td>Ali Mohammadi</td>
<td>HSE/EPR/BDP, World Health Organization, Geneva, Switzerland</td>
<td>Laboratory biosafety and biosecurity training course for Africa, Asia and Latin America</td>
</tr>
<tr>
<td>A70588</td>
<td>Hilary Ranson</td>
<td>Liverpool School of Tropical Medicine, UK</td>
<td>Insecticide resistance in African malaria vectors</td>
</tr>
<tr>
<td>A80361</td>
<td>Seydou Doumbia</td>
<td>Faculty of Medicine and Pharmacy, University of Bamako, Mali</td>
<td>Evidence basis for the improvement of integrated malaria vector control strategies in East, Central and West Africa</td>
</tr>
<tr>
<td>A70604</td>
<td>Pattamaporn Kittayapong</td>
<td>Mahidol University, Faculty of Science, Thailand</td>
<td>Innovative dengue vector control intervention and network based on novel tools and eco-bio-social strategies</td>
</tr>
<tr>
<td>A70585</td>
<td>Pablo Manrique-Saide</td>
<td>Universidad Autonoma de Yucatan, Mexico</td>
<td>Expanding targeted dengue vector control in Latin America: maximizing the potential of insecticide-treated materials</td>
</tr>
</tbody>
</table>

**Objective 3: Progressing Chagas disease vector control**

<table>
<thead>
<tr>
<th>Identification</th>
<th>Principal investigator</th>
<th>Institution</th>
<th>Project title</th>
</tr>
</thead>
<tbody>
<tr>
<td>A70596</td>
<td>Ricardo Gurtler</td>
<td>Universidad de Buenos Aires, Facultad de Ciencias Exactas, Argentina</td>
<td>Sources of reinestation by major vectors of Chagas disease after residual insecticide spraying</td>
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<tr>
<td>A80360</td>
<td>Maria Inés Picollo</td>
<td>Centro de Investigaciones en Plagas e Insecticidas, Villa Martelli, Argentina</td>
<td>Design and evaluation of complementary or alternative strategies for the control of Chagas disease vectors</td>
</tr>
</tbody>
</table>

**Coordination of BL5 activities**

<table>
<thead>
<tr>
<th></th>
<th>Institution</th>
<th>Activity</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>TDR secretariat</td>
<td>WHO-TDR, Geneva, Switzerland</td>
<td>Pls and SAC meetings, staff travel and coordination</td>
<td>Geneva, Switzerland</td>
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<tr>
<td>TDR secretariat</td>
<td>WHO-TDR, Geneva, Switzerland</td>
<td>Sixth meeting of the International Glossina Genomics Initiative and HAT project coordination meeting, 22–24 November 2008, Mombasa, Kenya</td>
<td>Geneva, Switzerland</td>
</tr>
<tr>
<td>TDR secretariat</td>
<td>WHO-TDR, Geneva, Switzerland</td>
<td>GM vectors projects coordination</td>
<td>Geneva, Switzerland</td>
</tr>
<tr>
<td>TDR secretariat</td>
<td>WHO-TDR, Geneva, Switzerland</td>
<td>Dengue projects coordination</td>
<td>Geneva, Switzerland</td>
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</table>

**Total** 2,489,114
<table>
<thead>
<tr>
<th>Funding in US$</th>
<th>Disease</th>
<th>Countries involved</th>
<th>Research area</th>
</tr>
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<tbody>
<tr>
<td>50 000</td>
<td>Malaria and dengue</td>
<td>Africa, Asia and Latin America</td>
<td>Capacity strengthening</td>
</tr>
<tr>
<td>199 700</td>
<td>Malaria</td>
<td>Angola, Benin, Burkina Faso, Chad, South Africa, Sudan and United Kingdom</td>
<td>Vector entomology, biotechnology and innovation</td>
</tr>
<tr>
<td>200 000</td>
<td>Malaria</td>
<td>Cameroon, Kenya, Mali, USA</td>
<td>Vector control, implementation research</td>
</tr>
<tr>
<td>150 000</td>
<td>Dengue</td>
<td>India, Indonesia, Myanmar, Philippines, Sri Lanka, Singapore, Thailand, United Kingdom, USA and Viet Nam</td>
<td>Vector entomology, implementation research</td>
</tr>
<tr>
<td>150 000</td>
<td>Dengue</td>
<td>Belgium, Brazil, Cuba, Guatemala, Mexico, United Kingdom, USA and Venezuela</td>
<td>Vector entomology, implementation research</td>
</tr>
<tr>
<td>243 600</td>
<td>Chagas disease</td>
<td>Argentina, Bolivia, Brazil, France, Paraguay and USA</td>
<td>Vector control</td>
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<tr>
<td>193 000</td>
<td>Chagas disease</td>
<td>Argentina, Bolivia, Colombia, France, Panama</td>
<td>Vector control</td>
</tr>
<tr>
<td>104 432</td>
<td>Malaria, dengue, HAT and Chagas disease</td>
<td>Disease-endemic countries worldwide</td>
<td>Vector entomology, capacity strengthening, biotechnology and innovation</td>
</tr>
<tr>
<td>44 952</td>
<td>Human African trypanosomiasis</td>
<td>Kenya, HAT community worldwide</td>
<td>Vector entomology, biotechnology and innovation</td>
</tr>
<tr>
<td>21 766</td>
<td>Malaria and dengue</td>
<td>Disease-endemic countries worldwide</td>
<td>Vector entomology, capacity strengthening, biotechnology and innovation</td>
</tr>
<tr>
<td>35 000</td>
<td>Dengue</td>
<td>Asia and Latin America</td>
<td>Vector entomology, capacity strengthening</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td></td>
<td></td>
<td><strong>2 489 114</strong></td>
</tr>
</tbody>
</table>
The Special Programme for Research and Training in Tropical Diseases (TDR) is a global programme of scientific collaboration established in 1975. Its focus is research into neglected diseases of the poor, with the goal of improving existing approaches and developing new ways to prevent, diagnose, treat and control these diseases. TDR is sponsored by the following organizations: