



TrypanoGEN: An integrated approach to the  
identification of genetic determinants of  
susceptibility to trypanosomiasis



[www.trypanogen.net](http://www.trypanogen.net)



# African Trypanosomiasis Associates with Tsetsefly Distribution



## Animal African Trypanosomiasis (AAT)

- ❖ *T. Vivax*
- ❖ *T. Congolense*
- ❖ *T. brucei brucei*

## Human African Trypanosomiasis (HAT)

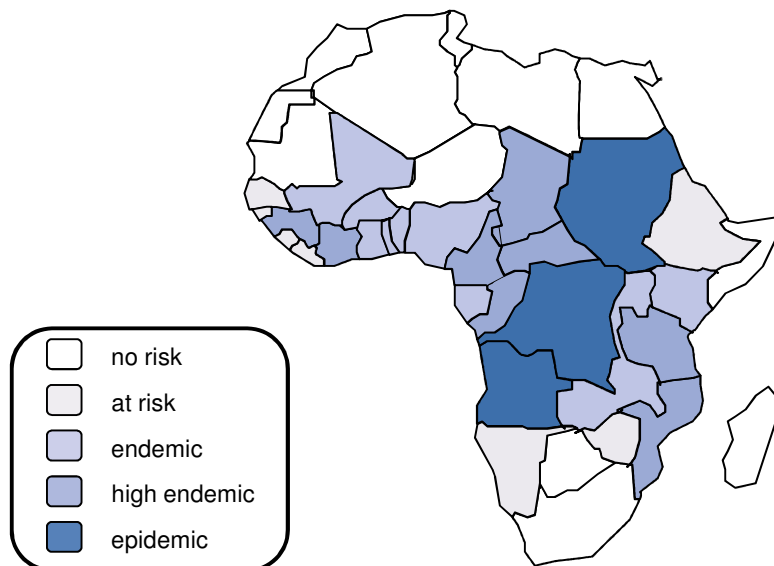
- ❖ *T. brucei rhodesiense*
- ❖ *T. b. gambiense*





# The problem

- HAT is a fatal neglected disease
- Estimated 70,000 human cases/year
- No vaccine
- Drugs are toxic
- Zoonotic - livestock cases estimated cost \$1.3bn/year
- Major impact on human and animal health





# New tools are needed

- Wide-spread consensus of the need for novel approaches to achieve elimination or sustainable control
  - New control strategies
  - New therapies



# The diversity of infection outcomes

OPEN ACCESS Freely available online



## Untreated Human Infections by *Trypanosoma brucei gambiense* Are Not 100% Fatal

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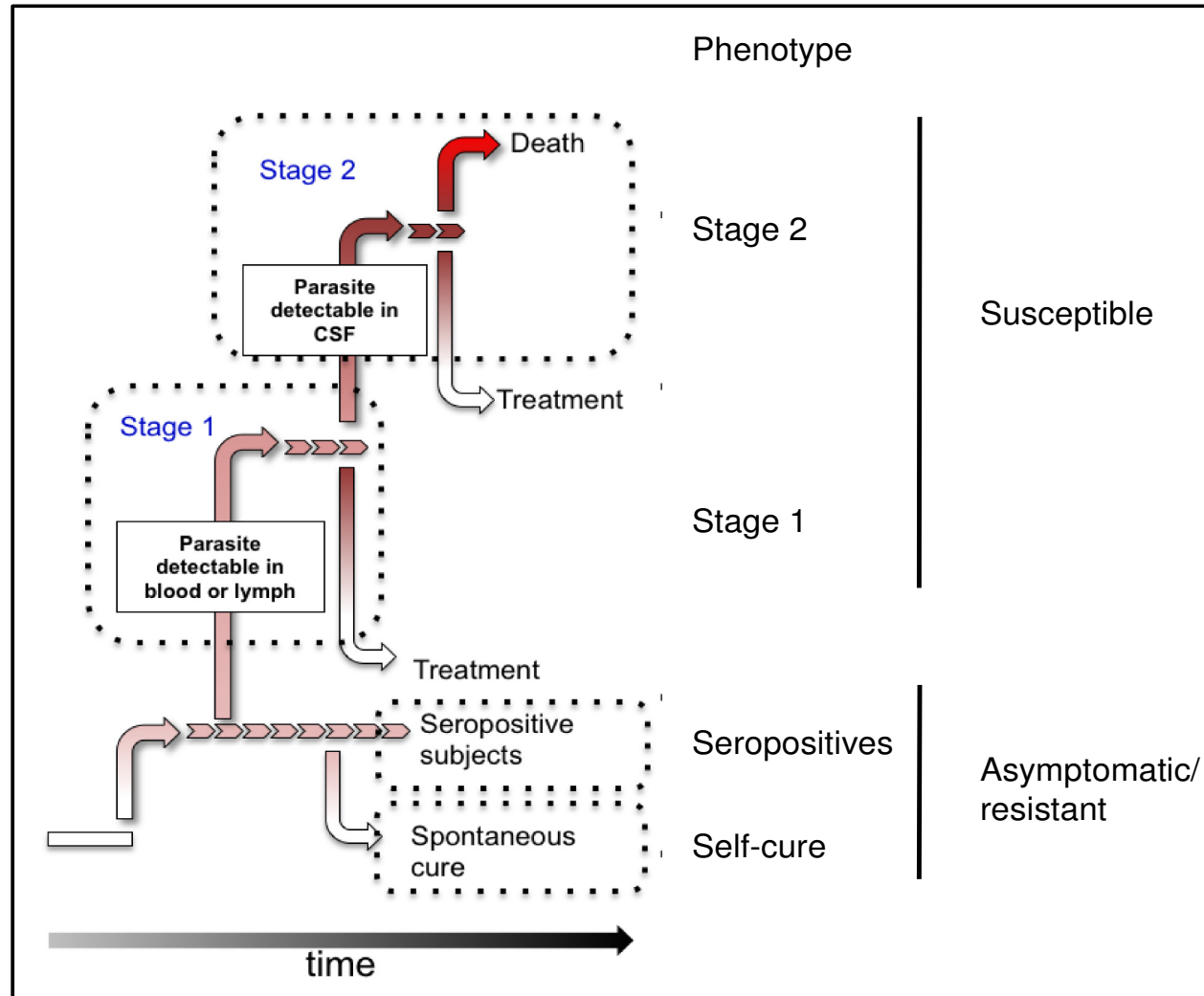
### Abstract

The final outcome of infection by *Trypanosoma brucei gambiense*, the main agent of sleeping sickness, has always been considered as invariably fatal. While scarce and old reports have mentioned cases of self-cure in untreated patients, these studies suffered from the lack of accurate diagnostic tools available at that time. Here, using the most specific and sensitive tools available to date, we report on a long-term follow-up (15 years) of a cohort of 50 human African trypanosomiasis (HAT) patients from the Ivory Coast among whom 11 refused treatment after their initial diagnosis. In 10 out of 11 subjects who continued to refuse treatment despite repeated visits, parasite clearance was observed using both microscopy and polymerase chain reaction (PCR). Most of these subjects (7/10) also displayed decreasing serological responses, becoming progressively negative to trypanosome variable antigens (LiTa 1.3, 1.5 and 1.6). Hence, in addition to the “classic” lethal outcome of HAT, we show that alternative natural progressions of HAT may occur, progression to an apparently





# The diversity of infection outcomes





# Research Question/Aim

**What are the host genetic determinants of HAT susceptibility/resistance?**

Exploit human genetic diversity to find the key to combating the disease:

In developing new control strategies

In developing new therapies



# Research Question and Objectives

## Objectives

- Create a network that systematically investigates genetic diversity in relation to HAT in endemic areas across Africa
- To create an extensive biobank of both retrospective and prospective samples with standardised parasitological and clinical metadata
- To generate a database of human genetic variation from different African countries
  - In order to identify loci associated with HAT susceptibility





# Hypothesis

**HAT per se is controlled by susceptibility/resistance loci and the GWAS that will be carried out in this project will reveal candidate loci for this phenotype.**



# Project overview

## The TrypanoGEN Biobank

### Existing samples

Controls	SERO	HAT
390	165	1060

### Minimum required for GWAS

Controls	SERO	HAT
600	400	1200

Year 1

Year 2

Year 3

Year 4

Year 5

### Activities

Biobanking existing samples  
Ethical agreement

WGS of 130 controls



Candidate gene testing

Design custom  
Omni2.5 Illumina

Genotyping  
2800 individuals

GWAS



Candidate gene testing

### Training

Ethics

Sampling/biobanking  
Sequence bioinfo

Ethics

NGS bioinfo  
SNPs arrays

Imputation meth.  
GWAS statistics

3<sup>rd</sup> Generation Seq  
Grantmanship



# Our GWAS plan

- To collect biological samples and clinical data from patients and controls.
  - At least 1000 cases
  - At least 1400 controls
- To conduct a GWAS
  - Sequence 130 individuals to obtain local SNPs
    - Focus on four regions:  
Uganda, DRC, Cote d'Ivoire, Guinea
  - Genotype ~half the samples (discovery cohort)
  - Genotype the rest for top 1% hits (validation cohort)



# Details of GWAS

Re-sequencing of African population  
N=130 from the 4 centres

Output: To inform SNP imputation



Genotyping  
**Discovery cohort**  
Stage 2 patients N=600  
Asymptomatic controls N=200  
Population controls N=500

Output: Top hits



Genotyping of 1% top hits  
**Validation cohort**  
Stage 2 patients N=400  
Asymptomatic controls N=200  
Population controls N=900



# Case and Control definitions

## Cases

- Individuals confirmed as HAT infected by demonstration of Trypanosomes in, blood, Lymph or cerebrospinal fluid

## Controls

- Living in same villages as cases
- No Trypanosomed demonstrated in any body fluids
- Serologically negative
- Species specific PCRs to confirm negativity



# Who/where we are

9 African + 3 European countries



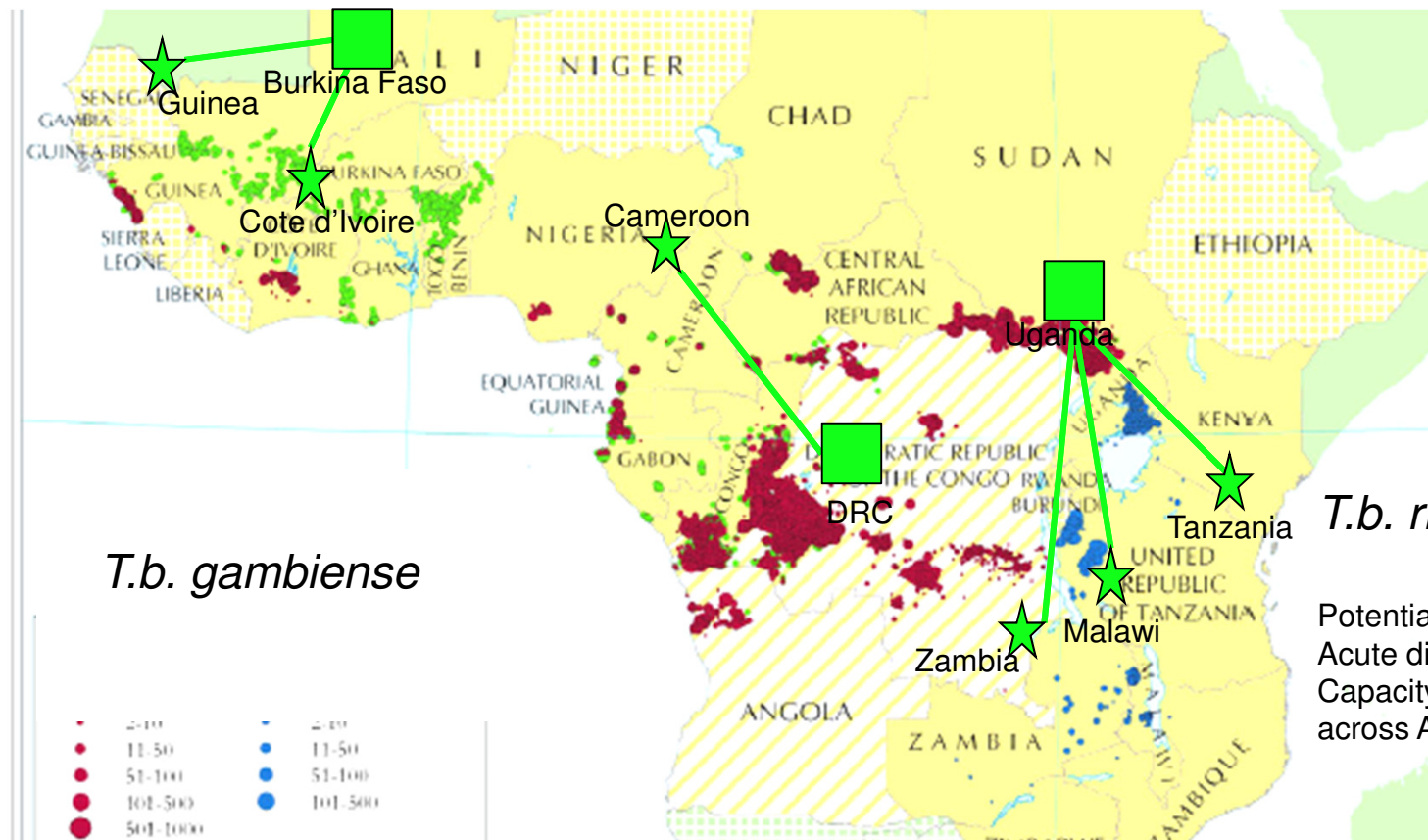
UK



France



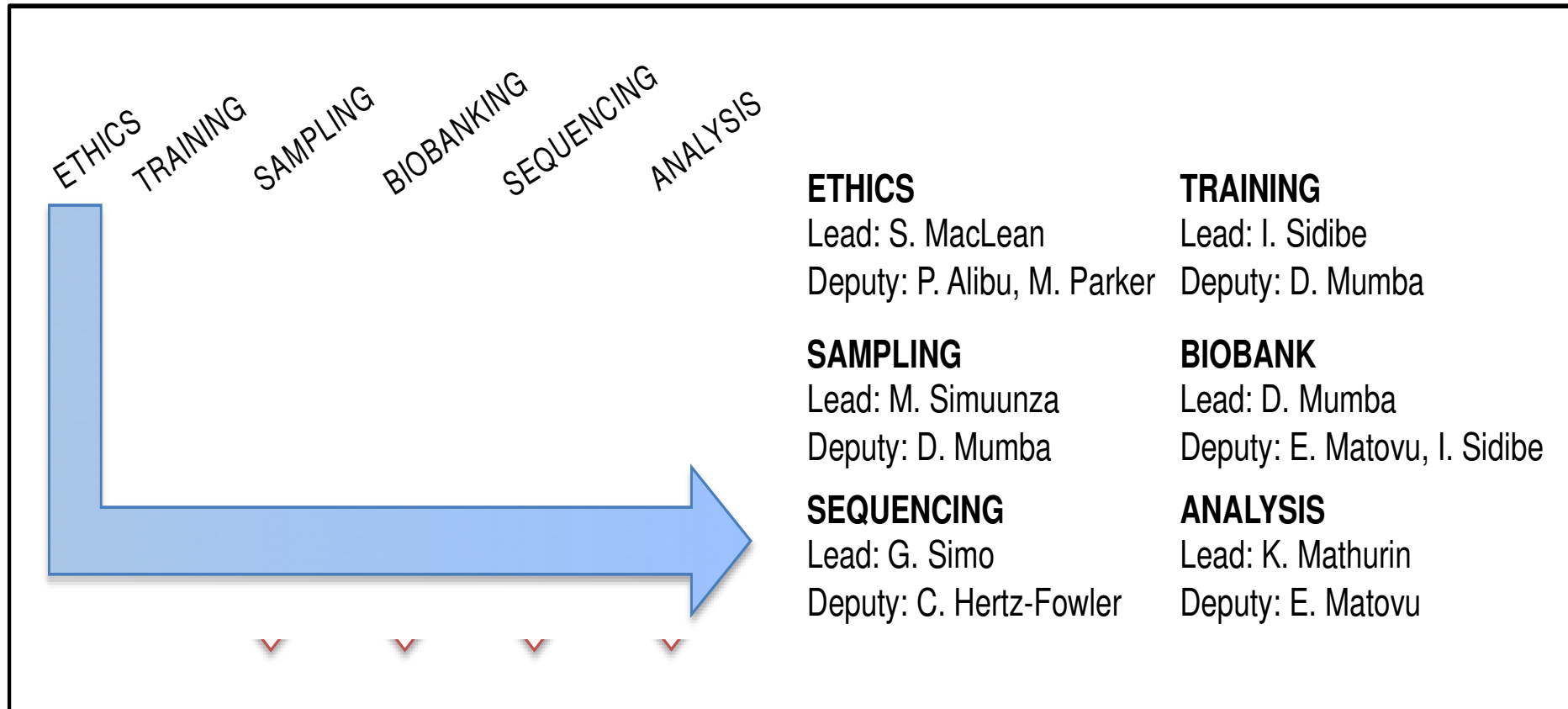
Belgium





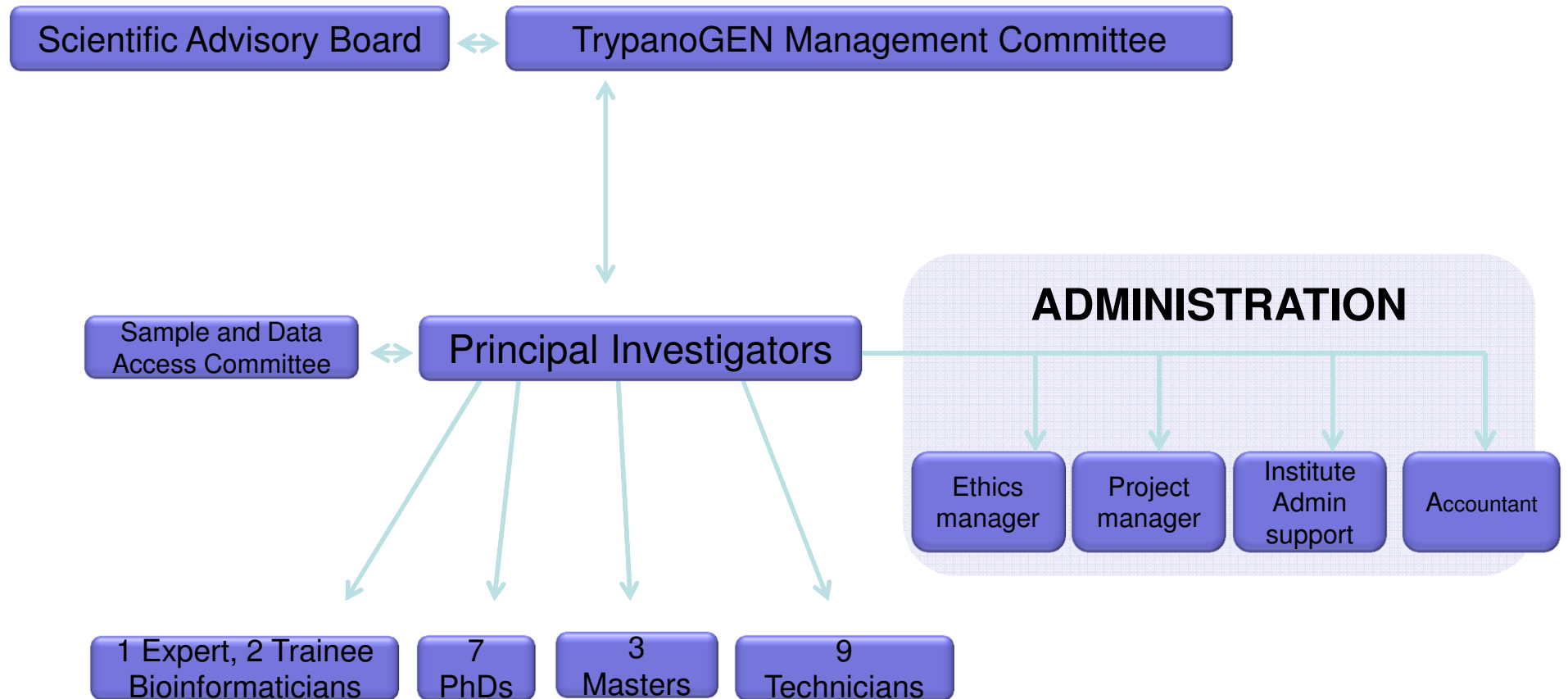


# Ensuring delivery





# Ensuring delivery





## Areas of potential synergy with other H3 Africa networks

- Ethics
- Training
  - grantsmanship
  - bioinformatics and GWAS (H3ABionet)
  - ethics workshops
- Sharing data policies
- Shared samples (Kidney Disease)
  - SNP database
- Logistics
- Infrastructure building
- Communication across Africa



## Developments since the Award

- Visit by WT finance team to Makerere University February 2013
- Ethical review (MoH) and recommendation to UNCST
- Ethical approval Granted
- Kick off meeting in Kampala 28-31 May 2013
- Training finance team from participating institutes



# Developments since the Award

- Sub-Awards Issued
- Funds transfer just began
- SOPs for sample collection/storage in place
- Sample collection in DRC started (78 cases so-far)
  - Uganda, Cameroon, CIRDES to start October-December
- Piloted with DNA preparation kits
  - Blood
  - Saliva



# Streamlining consent documents

- 4 examples on data/sample sharing

	<b>Approved?</b>	<b>Data</b>	<b>Sample</b>	<b>Remarks</b>
Uganda	Yes	X		Protocol amendment to specify sample sharing underway
DRC	Yes	X	X	
Zambia	Under Review	X	X	
Malawi	Under Review	X	X	





## On-going activities

- Recruit key personnel
  - Study coordinator application under review
  - Expert bioinformatician
- Finalise sub-awards and funds transfer
- Formally recruit identified PhD students
- Workshop on sample processing, storage and DNA extraction

**We are challenged by poor intra-network communication!**