

PERSONAL INFORMATION **OBARA ISAAH OTIENO**

📍 International Livestock Research Institute, Old Naivasha Road, P.O. Box 30709, 00100 Nairobi (Kenya)

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Sex Male | Date of birth 03 January 1982 | Nationality Kenyan

WORK EXPERIENCE

2011–Present **PhD candidate**

DFG German-African Cooperation Projects in Infectiology  
Molecular epidemiology network for promotion and support of delivery of live vaccines against *Theileria parva* and *Theileria annulata* infection in Eastern and Northern Africa, Borstel (Germany)  
[http://www.dfg.de/en/magazine/dfg\\_international/research\\_africa/](http://www.dfg.de/en/magazine/dfg_international/research_africa/)

2009–2010 **Research consultant**

Kenya Arid and Semi-Arid Research programme (KASAL), Kenya Agricultural Research Institute (KARI), Nairobi (Kenya)  
<http://www.kari.org/>

Identification of *Streptococcus agalactiae* protective antigens (surface immune protein and pilin components) by whole genome screening

2008–2009 **Msc candidate**

The WellcomeTrust Host Pathogen Project, University of Liverpool, UK and Livestock Research Institute (ILRI), Nairobi (Kenya)  
<http://www.genomics.liv.ac.uk/tryps/>

Functional genomics of host tolerance and host pathogen interactions in vector borne parasitic diseases of cattle: use of a combination of genetic and in vitro analysis to assess the differences between susceptible Boran and tolerant N'Dama cattle in their response to infection with *T. congolense*

2011–2013 **Teaching experience**

Kenyatta University, P.O. Box 43844 , Nairobi (kenya)  
<http://www.ku.ac.ke/>

Undergraduate courses in Immunogenetics, Population Genetics and Principles of Animal Breeding

EDUCATION AND TRAINING

2011–Present **PhD**

University of Lübeck, Ratzeburger Allee 160 23562 Lubeck, (Germany)  
<http://www.uni-luebeck.de/en/universitaet.html>

Thesis title: Diversity of molecular alterations and selective pressures underlying bovine adaptive immune responses to the lymphoproliferative protozoan parasite *Theileria parva*

Project aims:

Determine the extent of B cell-epitope polymorphism and amino-acid sites showing the most potent signatures of selection on the major *T.parva* sporozoite surface antigen *p67* from clinically reacting cattle at the *livestock-wildlife interface*

Establish a pipeline for next generation sequencing of the entire cattle MHC region with a particular emphasis on refinement of the class I variability

*In silico* prediction of epitopes and *ex vivo* determination of the breadth of T cell responses to *T. Parva* schizont candidate antigens to reveal putative proprietary MHC -I specificities in African taurine cattle

2007–2009 **Master of Science (Msc) Immunology**

Kenyatta University, P.O. Box 43844 , Nairobi (Kenya)  
<http://www.ku.ac.ke/>

Thesis: Association between genotypes at polymorphisms in the trypanotolerance candidate gene, *ARHGAP15* (Rho GTPase-activating protein 15) and the pathophysiology of trypanosomiasis associated anaemia.

Project aims:

Screen an EST library for nonsynonymous SNP in genes within the QTL for parasitemia, body weight, and packed cell volume after *T. congolense* infection in a Boran x N'Dama F2 cross.

Express the two *ARHGAP15* alleles (282 H→P) *in vitro*

Determine if the nonsynonymous sequence difference in the *ARHGAP15* gene is playing an important role in the differences between susceptible Boran and tolerant N'Dama cattle in their response to infection with *T. congolense*.

Relevant courses/Grade:

Molecular Immunology and Immunogenetics (A)  
Immunohaematology (A)  
Clinical Immunology (A)  
Immunology of Parasitic and Infectious Diseases (A)  
Reproductive Immunology (A)  
Immunochemistry (B)  
Experimental Design and Statistics (A)  
Cellular Immunology (A)  
Immunochemical Techniques (A)

2001–2005 **Bachelor of Education Science**

First class honors

Kenyatta University, P.O. Box 43844 , Nairobi (Kenya)  
<http://www.ku.ac.ke/>

Relevant courses/Grade

Advanced Genetics (A)  
Advanced Immunology(A)  
Applied Immunology(A)  
Cell Biology and Genetics(A)  
Biostatistics(A)  
Fundamentals of Immunology(A)  
Essentials of Cell Biology(A)

2011–2014 **Supplementary courses**

October 2013

Advanced Bioinformatics training workshop. Beca-ILRI Hub (Nairobi) in collaboration with Swedish University of Agricultural Sciences (SLU), Sweden.

June 2013

Immunological Bioinformatics Summer School, Center for Biological Sequence Analysis, Technical University of Denmark

April 2013

Introduction to the Epidemiology Toolbox Workshop, International Animal Health , Faculty of Veterinary Medicine, Freie Universitaet Berlin, Germany

November 2012

Scientific Research Paper Writing Workshop, International Livestock Research Institute, Addis Ababa, Ethiopia

March 2012

Technical Workshop on Bioinformatics, Veterinary Infection Biology, Research center Borstel, Germany

October 2011

Advances in the Knowledge of Parasite Resistance of Ruminant Hosts and Parasites Course, Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil

**ADDITIONAL INFORMATION****Publications****Peer-reviewed journal articles:**

Noyes, HA; Brass A; **Obara, I**, Anderson, SI; Archibald, AL; Bradley, DG; Fisher, P; Freeman, AR; Gibson, J; Hall, L; Hanotte, O; Hulme, H; McKeever, D; Murray, C; Oh, SJ; Rennie, C; Smith, K.C.; Tapio, M., Wambugu, J; Gicheru, M; Williams, D; Kemp, SJ; Agaba, M (2010). Genetic and expression analysis of cattle identifies TRIF and AHRGAP15 as candidate QTL genes in pathways responding to infection with *Trypanosoma congolense*. *Proc. Natl. Acad. Sci*

**Obara I**, Ulrike Seitzer, Kemp Stephen , Musoke Tony, Spooner Paul, Ahmed Jabbar , David Odongo , Joana C. Silva, Richard P. Bishop (2014). Molecular evolution of epitopes recognized by antibodies on the *T. parva* p67 sporozoite antigen. *Parasitology*, in press.

**Journal articles in preparation**

**Obara I**, Svitek N, Ulrike Seitzer, Kemp Stephen, Ahmed Jabbar , *Elías Awino*, Nene V, Richard P. Bishop . *In silico* predicted epitopes and *ex vivo* determined breadth of T cell responses to *T. Parva* shizont candidate antigens reveal putative proprietary MHC -I specificities in Ankole cattle. In preparation for submission to *Immunogenetics*

**Obara I**, Nielsen M, Svitek N, Ulrike Seitzer, Kemp Stephen, Ahmed Jabbar , *Elías Awino*, Nene V, Richard P. Bishop. Co-occurrence and mutual exclusivity of gene mutations at the peptide binding region of MHC class I alleles between the African cape buffalo (*Syncerus caffer*), the major wildlife reservoir of *T. parva* and cattle. In preparation for submission to *Immunogenetics*

#### Published Abstracts:

**Obara I**, Noyes H, Gicheru M, Agaba M, Kemp S (2011). ARHGAP15 allelic heterogeneity and the pathophysiology of trypanosomiasis associated anaemia. Advances in the Knowledge of Parasite Resistance of Ruminant Hosts and Parasites Course, Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil

**Obara I**, Noyes H, Gicheru M, Agaba M, Kemp S (2010). Genotypes at polymorphisms in the trypanotolerance candidate gene ARHGAP15 and the pathophysiology of trypanosomiasis elicited anaemia. International symposium on animal Genomics for Animal Health, 31 May - 2 June 2010, PARIS (FRANCE), Poster Abstract

**Obara I**, Noyes H, Gicheru M, Agaba M, Kemp S (2009). Characterization of Trypanotolerance Candidate Genes: Determination of the Kinetic Parameters of ARHGAP15 Allelic Variants Stimulated RAC1-GTP Hydrolysis. Plant & Animal Genomes XVII Conference San Diego, CA

**Obara I**, Noyes H, Gicheru M, Agaba M, Kemp S (2009). Association between genotypes at polymorphisms in the trypanotolerance candidate gene ARHGAP15 and the pathophysiology of trypanosomiasis associated anaemia (2009). Biosciences eastern and central Africa (BecA), ILRI Hub and Syngenta Foundation for Sustainable Agriculture Partnership Conference: From technology to product development for the African farmer

#### Technical skills And competences

##### Bioinformatic and statistical research experience:

Hands-on experience with analysis of high-throughput omics data, such as next-generation sequencing data

*In silico* prediction of T and B cell epitopes by Position-specific scoring matrices (PSSMs) and Artificial neural networks (ANNs)

Experience in phylogenetic inference and explicit detection of codons with potent signatures of positive selection

Linux/Unix and High Performance Computing experience

Basic understanding of Perl programming and R/Biocoductor software package

##### Molecular biology:

Substantial experience in molecular biology techniques including genetic engineering and protein expression, and adaptor ligation, library amplification by emulsion PCR, and pyrosequencing

##### Immunoassays

Expertise in *ex vivo* ELISPOT assay, ELISA and Western blotting

##### Personal skills

Good verbal and written communication skills and ability to work well with multi-disciplinary teams

References **Dr. Richard Bishop**  
Principal Molecular Biologist  
International Livestock Research Institute (ILRI)  
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