Welcome to the 6th edition of the Urban Zoo Newsletter and hopefully you all have ushered in New Year 2015 with renewed enthusiasm and energies to drive Urban Zoo to new heights of success.

Although any medical research project has many components, no doubt in aspects of Urban Zoo the microbiological analyses play a central role in providing answers to questions that we face in the field during interrogation of study environments and populations. This applies to both cases and control populations as well as interaction with their environment. We are keen to ensure that the results from our laboratories will be of high quality and will provide the required component to health solutions for the populations that we seek to help.

In summary to-date, from one part of the study alone, we have processed a total of 683 faecal swabs for enteric bacterial and viral pathogens and including 411 from Korogocho and 272 from Viwandani. From these samples, a total of 537, (315 from Korogocho and 222 from Viwandani) E. coli isolates were obtained and archived so far. Other enteric pathogens which were isolated were; Salmonella isolates 20. Shigella isolates 8. V. cholerae isolates 3. Campylobacter isolates 9. E. fergusonii 1. Enterobacter agglomerans 1 and Aeromonas hydrophila 1. In parasitology a total of 683 faecal samples was processed parasites detected; E. histolytica 77, G. lamblia 130, A. lumbricoides 20, H. nana 5, T. trichiura 9, Fasciola spp 1, Hookworm 4.

Antimicrobial sensitivity testing (AST) was performed on 537 E. coli isolates using 13 antimicrobials including kanamycin, nalidixic acid, chloramphenicol, trimethoprim/sulfamethoxazole, ciprofloxacin, gentamicin, streptomycin, amoxicillin/clavulanic acid, cefazidime, tetracycline, ceftriaxone, ampicillin and cefuroxime. 33 (6%) E. coli isolates were found to be resistant to ciprofloxacin (CIP) and 25 (5%) E. coli isolates were resistant to ceftriaxone (CRO), which form a few of the last line of defense for severe Gram negative bacterial infections. These are critically important and rare antimicrobial resistant phenotypes especially as these bacteria were that were also resistant to several other commonly available drugs.

In 2014, Antimicrobial Resistance (AMR) was declared a global emergency by the World Health Organization. As we seek answers on ways to minimize emergence and spread of AMR in our study populations, we are reminded that certain sections of the populations overuse antimicrobials while others have no access to these life-saving agents. Further microbiological and genomics analysis will provide answers as we seek to understand the population dynamics and genetic basis/transmission potential of this phenotype.

My commendations to the KEMRI and UoN lab teams for a job well done so far!

Sam Kariuki is Director of the Centre for Microbiology Research at the Kenya Medical Research Institute (KEMRI) and co-ordinator of the postgraduate Medical Microbiology Course hosted by the Institute in Nairobi.
At dawn as the sun rose above the jagged peaks of Nyambene hills, Fred Amanya and I would trudge our way out to Isiolo town towards Mlango area or Kachuru or Gotu. The journey along the dusty roads would be occasioned by chats concerning the security situation and the serious drought in the county as “taarab music” played mellifluously in the stereo.

Brucellosis is a zoonotic disease transmitted to humans mainly by consumption of raw milk and physical contact. Unfortunately, there is lack of quantitative understanding of the scale of the disease in camels in Kenya. This is further exacerbated by consumption of raw camel milk owing to the presumed associated health benefits and other social cultural believes. In this regard we undertook a study to explain this phenomena.

By the time we arrive the camel workers are up preparing the camels for milking, we set up our temporary station under a dry acacia tree. We collect milk, blood, nasal swabs and fecal samples randomly from the camels. Restraint of camels proved to be quite grueling especially for the big bulls and some young ones who tend to be wild. This however proves to be an easy challenge for the camel herders who have been born and raised in camel keeping families. We finish our work by 10:00 am and our journey back to Isiolo was a quiet one courtesy of the hot sun.

Upon arrival at the laboratory in Isiolo town the milk samples were analyzed for brucellosis using modified Milk Ring Test. All other samples were processed and kept in the freezer for transport to the ILRI laboratory in Nairobi where they will be tested for brucellosis. Nasal swabs, EDTA and serum will be forwarded for testing by collaborators.

The day comes to close at 4:00pm with a cold shower and glass of camel milk (not the collected samples definitely.) During our two-week stay we managed to visit sixteen camel herds and collected more than 200 samples. However, on one of the days our still voyage came to a halt for two hours after our car got stuck in a hyena den.

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A tapeworm found in humans but acquired through eating infected pork (*Taenia solium*), has been linked to acquired epilepsy in humans. The larvae stage of the tapeworm causes a disease called Cysticercosis both in pigs and humans characterised by formation of cysts in muscles. When people consume viable cysts from infected pork, the ingested larvae matures into adult tapeworm which again produces eggs that are released into the environment. Infection in both pigs and humans is acquired through accidental ingestion of human faeces containing *T. solium* eggs or consumption of contaminated food or water. The diagram below shows the life cycle of *Taenia solium*.

### Important facts about Cysticercosis

- It can cause neurocysticercosis, which is the leading cause of acquired epilepsy
- It is ranked by Food & Agriculture Organisation (FAO) & World Health Organisation (WHO) as the most important zoonotic foodborne pathogen in the world.
- It does not show obvious clinical signs, so it is not easy to detect. Therefore the disease may be transmitted for several months or years before detection.
- Previous studies in Homa-Bay and Busia, Kenya has confirmed the presence of this disease in the Kenyan pigs, but national prevalence of the disease in both pigs and people is lacking.
- People who suffer from epilepsy are often marginalised as there are several myths trying to explain the cause.

### What Urbanzoo Project is doing about Cysticercosis:

#### Serological survey of porcine cysticercosis in pigs slaughtered at Ndumbuini abattoir in Nairobi, Kenya

The main objective of the study is to estimate the risk of cysticercosis infected pork entering the Nairobi food system for consumption. We are collecting blood samples from pigs presented for slaughter, then testing for cysticercosis using Antigen ELISA and estimating the prevalence. Focus Group Discussions (FGD) and individual interviews are conducted to gather information for mapping the pork value chain and assess the risk of consuming *T. solium* infected pork from Ndumbuini abattoir (*This will form part of the MSc. research project for James Akoko-Author of this article*).

#### Neurocysticercosis and Epilepsy study in Busia

A sub-set of the project team is currently in Busia on an associated project in collaboration with the University of Yale, USA, collecting blood samples from people and pigs for serological testing for cysticercosis. A questionnaire and clinical examination is conducted to identify possible cases of neurocysticercosis, who are then taken to Agakhan hospital in Kisumu for CT scan. The main objective of this study is to try and understand the contribution of neurocysticercosis in epilepsy cases in western Kenya.

*Article written by James Akoko, Field Coordinator for Urban Zoo Project, working on Cysticercosis as part of his MSc research Project.*
THE POWER OF NEXT GENERATION SEQUENCING

The power of next generation sequencing is allowing us to gain a more detailed understanding than ever before about how bacteria spread. I am hugely excited to be a part of the Urban Zoonoses project, which will generate a vast amount of bacterial isolates along with metadata at an unprecedented level of detail.

We will be performing whole genome sequence analysis of bacterial samples collected through many strands of the Urban Zoonoses project, from humans, livestock, food, wildlife and the environment. I will use state-of-the-art methods for integrating the bacterial genetic sequence data with information about the time, location and host from which the bacteria were sampled. By combining epidemiological and demographic information with the genetic data, we will be able to understand the E. coli diversity within Nairobi, and how this differs across socioeconomic groups, in different housing types and in relation to livestock keeping practices.

From the bacterial genome sequences we can also look for genes of interest, such as those conferring bacterial virulence or resistance to antibiotics. By examining the set of genes carried by bacteria from different individuals, hosts or locations, we can make inferences about reservoirs of antibiotic resistance and pinpoint potential hotspots for disease outbreaks, with a particular emphasis on zoonotic transmissions.

I have previously used whole genome sequence analysis to investigate the transmission of S. aureus between livestock and humans, and have also used phylogenetic techniques to help understand the origins of the HIV-1 group M epidemic. I am currently assessing the utility of whole genome sequencing as a tool for identifying epidemiologically related E. coli infections in collaboration with the Scottish E. coli O157 Reference Laboratory.

My involvement with the Urban Zoonoses project is made possible through a Junior Research Fellowship at the Centre for Immunity, Infection and Evolution at the University of Edinburgh, and a Sir Henry Wellcome Postdoctoral Fellowship from the Wellcome Trust.

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