

## SEMINAR ANNOUNCEMENT

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## SEMINAR ANNOUNCEMENT

Submitted by pmakenzi on Tue, 2017-06-20 11:23

**Date and time:** Tue, 2017-06-20 10:43

**Location / Venue:**

ANIMAL PRODUCTION LECTURE THEATER

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**UNIVERSITY OF NAIROBI**

**FACULTY OF VETERINARY MEDICINE**

**DEPARTMENT OF ANIMAL PRODUCTION**

**Degree: Master of Science in Animal Genetics and Breeding****Title:** "METAGENOMIC ANALYSIS OF ENTERIC PATHOGENIC MICROORGANISMS AFFECTING THE PERFORMANCE OF SMALLHOLDER DAIRY COWS IN KENYA AND TANZANIA"

**By: Vincent Habimana (J56/80626/2015)**

**Title:** "GENETIC DIVERSITY OF MAJOR HISTOCOMPATIBILITY COMPLEX (MHC) IN LOCAL CHICKEN ECOTYPES IN KENYA"

**By: Njau Wanjahi (J56/781744/2015)**

**Venue:** DEPARTMENT OF ANIMAL PRODUCTION LECTURE THEATRE

**DATE: WEDNESDAY 21st June, 2017**

**Time: 2.15pm-3.15pm.**

### **METAGENOMIC ANALYSIS OF ENTERIC PATHOGENIC MICROORGANISMS AFFECTING THE PERFORMANCE OF SMALLHOLDER DAIRY COWS IN KENYA AND TANZANIA**

**By:** Vincent Habimana (J56/80626/2015)

#### **Abstract**

Bovine ruminant particularly dairy cow contributes to the nutrition and well-being of humans by providing a variety of dairy products. Milk production is of great economic concern to farmers and its quality is closely associated with the health of human beings. Improving its production relies on ruminant research; understanding of the microbial organ of dairy cows. Dairy cows evolve a symbiotic relationship with a complex microbiome composed of bacteria, viruses, protozoa and fungi which are responsible for the microbial digestion of plants' derived feed resources. The molecular characterization of the rumen microbiota is a viable option in studying the micro-organisms with regards to their effects on performance of dairy cows. Dairy animals consume large quantities of fodder consisting of a wide variety of microorganisms which can be pathogenic or non-pathogenic. Those pathogens found in the rumen nutrients are absorbed in the blood system. This predisposes the dairy cow to the reproductive tracts infections such as mastitis and retained placenta. This causes the significant impact on the profitability of the dairy industry because of lowered reproductive efficiency, decreased milk production and infertility in animals. The procedures for detecting those pathogens vary according to the target microorganisms, clinical examinations require a variety of media, reagents and culture methods which is laborious in nature and time consuming. In addition, different bacteria have different growth requirements and fail to grow in a given culture medium. We are therefore depending on antimicrobials for the treatment of dairy

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cattle affected with pathogenic microorganisms. It is known that the use of these antimicrobials in dairy cows benefit the development of resistant strains in the host animals. However, little is known about the diversity, distribution and origins of resistant genes, especially unculturable majority of environmental bacteria. Therefore, the use of rapid sequencing technologies combined with molecular methods is becoming a gold standard for evaluating the microbiomes of animals. In this regard, metagenomics, the genomic analysis of a population of microorganisms makes possible the profiling of microbial communities in the environment. Metagenomics allows the identification and characterization of the composition of microbiota as well as the abundance of their genes. The project undertakes to detect and genetically characterize enteric pathogenic microorganisms affecting the performance of smallholder dairy cows in Kenya and Tanzania using metagenomics approaches and assess antimicrobial resistant potential for the detected strains. This will give information on the composition of pathogenic microorganisms present in the rumen of the dairy cow. Therefore, the study will provide also the novel intervention strategies and appropriate detection techniques for genes resistant to antimicrobials in dairy cows.

### GENETIC DIVERSITY OF MAJOR HISTOCOMPATIBILITY COMPLEX (MHC) IN LOCAL CHICKEN ECOTYPES IN KENYA

By: Njau Wanjau (J56/781744/2015)

#### Abstract

Local chicken ecotypes in Kenya show extensive physical diversity due to their ability to thrive in different ecological zones under varying climatic conditions. They are raised under scavenging conditions with a high predisposal of parasites and diseases. In order to survive they have to display fitness in their immune related genes. Chicken major histocompatibility complex (MHC) consists of several clusters of highly polymorphic genes associated with disease resistance. The diversity of MHC in the Kenyan local chicken ecotypes has been done using microsatellite markers which under estimate genetic divergence and accurate scoring of polymorphisms. There is little information showing existence of chicken with resistance genes to any common poultry diseases. The study aims to improve local chicken ecotypes disease resistance and conservation by assessing genetic diversity in MHC region, and of specific genes within MHC responsible for immune response and disease control using next generation sequencing. Blood samples will be collected from eight regions in Kenya (48 birds per region) namely; Kakamega, West Pokot, Siaya, Turkana, Bomet, Narok, Lamu and Taita Taveta. Genomic DNA will be extracted by use of phenol chloroform and whole genome sequencing done by illumina. Extraction of SNPs will be done by variant calling pipeline. Population parameters such as heterozygosity, nucleotide diversity, haplotype diversity will be analyzed and linkage disequilibrium. MHC genes will be annotated to amino acids where diversity will be assessed at nucleotide and amino acid level. MHC genes are useful molecular markers for assessing status of endangered populations hence the study will evaluate the risk status of local chicken populations in Kenya

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Attachment	Size
<a href="#">MSc Proposal presentation memo wednesday 21st June 2017.pdf</a>	2.03 MB

**Source URL:** <http://animalproduction.uonbi.ac.ke/node/45376>

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