

## SESSION 10: Viral Genomics and Bio-informatics

### SESSION 10: VIRAL GENOMICS AND BIO-INFORMATICS

**Organizer: Dr. Appolinaire Djikeng -, ILRI**

**Chair: Dr. George Michuki**

#### ORAL PRESENTATIONS

##### 1. Evaluating the risk of spread of H5N1 highly pathogenic avian influenza in Kenya

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##### **Abstract**

Outbreaks of H5N1 highly pathogenic avian influenza (HPAI) occurred in 11 countries in Africa between the years 2006 – 2008. Kenya did not get exposed to the disease but as the perceived risk of introduction of the HPAI virus heightened, the demand for poultry and poultry products waned. This resulted in enormous economy-wide impacts. To generate information that could be used for improving the contingency plans that had been developed by the Department of Veterinary Services, we assessed the risk of spread of the disease in the country using a spatial simulation model; the model used data on topography, landscape features, and vegetation and road networks in a spatial lattice of 1 square km. We also conducted a parallel qualitative risk assessment study involving small scale commercial (sector 3) and backyard (sector 4) poultry farms to identify poultry production practices that

could be associated with the release or exposure of the virus at the farm-level. The model identified the ports of Mombasa and the JKIA as potential gateways of introduction of the disease. It also revealed that densely populated areas, e.g. cities, had higher risk of experiencing outbreaks compared to sparsely populated ones. Similarly, areas that have dense road networks had higher risk of experiencing outbreaks. Qualitative risk assessment studies indicated that the risk of transmission of the disease from an infected backyard farm was higher than that from an infected small scale commercial farm due to poor biosecurity practices found on such farms. Free-range production systems in backyard poultry farms, for example, allow unlimited contact between poultry and “farm-bridge” animals and birds. These studies identified geographical zones and farm practices that should be targeted for surveillance. They also identified areas for further research

##### 2. Molecular epidemiology of foot-and-mouth disease in East Africa: the challenges of disease control in an endemic region

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##### **Abstract**

Foot-and-mouth disease (FMD) is an acute and highly contagious disease of domestic and wild cloven-hoofed animal species; with direct social and economic consequences. The governments of the East African region spend large amounts of money in their annual national budgets towards the control of FMD. FMD is endemic in many parts of East Africa, with the number of outbreaks increasing every year. In this presentation I review the contribution of small ruminants and wildlife to the maintenance of FMD in the region, the effectiveness of current vaccination strategies in the

region, cross-border movement of FMD in and beyond the region, and possibilities for FMD viral evolution and recombination in East African. The results in the work reviewed have been produced through the use of molecular epidemiology and serological approaches. Recent results show that small ruminants are seropositive and may contribute the presence of FMD. The additional seropositivity of African buffaloes in the different national parks in Uganda suggests that these too may play an important role in the epidemiology of SAT serotypes of FMDV. Indeed this is in contrast with the predominant serotypes in cattle around the

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national parks. Molecular analyses point towards possible ineffectiveness of currently used vaccines, and possibilities of cross border introductions of FMD. These observations highlight the importance of concerted regional approaches to the control of trans-boundary animal diseases such as foot-and-mouth disease.

**Keywords:** foot-and-mouth disease, serotype O, SAT serotypes, molecular epidemiology, disease control.