

## Understanding pathogen, livestock, environment interactions involving bluetongue virus: the PALE-Blu



The International Livestock Research Institute (ILRI) recently received funding from the European Union (Horizon 2020), in partnership with scientists from 19 different research institutes and universities around the world, to investigate the prevalence and the diversity of circulating BTV serotypes in key regions of sub-Saharan Africa. ILRI's part of the study is to collect samples from different animal species present in different countries of Africa where BTV data is lacking. Emphasis will also be placed on an in-depth understanding of the prevalence of the virus in different agroecological zones in Kenya.

Analysis of the samples will include ELISA to measure anti-BTV antibodies indicating prior exposure to the virus, quantitative PCR (qPCR) to assess the level of ongoing infection, and molecular typing by qPCR to identify the most prevalent circulating serotypes in these regions. BTV isolation on insect cells will also be attempted from positive field samples to eventually generate a biobank of BTV field isolates from the sub-continent. These virus strains can then be used for further characterization by next-generation sequencing, or for pathogenesis, transmission and vaccination studies at ILRI and with international partners.

The data generated from this study will shed more light on the status of BTV in sub-Saharan African and will hopefully lead to strategies for a better control of the disease in the future.

### Key messages

Bluetongue virus (BTV) is widespread in sub-Saharan Africa and causes a disease that mainly affects sheep.

Bluetongue (BT) can cause substantial economic losses due to fatalities of livestock, or due to ban on the livestock trade between countries.

A better understanding of the circulating serotypes in Africa, spread dynamics of the virus, and the development of a multivalent vaccine towards BTV will allow for a better control and prevention of future outbreaks.

ILRI recently received funding to investigate on the current circulating BTV serotypes in sub-Saharan Africa

### The disease

Bluetongue (BT) is a vector borne disease caused by the bluetongue virus (BTV) that affects livestock such as sheep, goat or cattle. It can also infect wild animals such as antelopes, deer and wildebeest, to name a few. The disease is most severe in sheep and can result in death. The causative agent of this disease is an Orbivirus member of the Reoviridae family, a virus family in which the human pathogens reovirus and rotavirus are also found. Cattle are the principal reservoir of BTV but usually do not develop clinical signs of the disease.

The clinical signs of the disease manifests within 5–10 days post infection and include fever; swelling of the face, lips and tongue; breathing difficulties; and sores on the muzzle and gums. Reddening will also be observed on the mucosal membranes of the eyes, nose and mouth. The severity of the disease varies depending on the viral strains, the animal species and the environment.

To date, there are 27 serotypes of BTV that have been identified and new types are still being discovered. This virus is transmitted by *Culicoides* biting midges and is thus rightly called an arbovirus. However, some serotypes are transmitted without the help of the arthropod vector.

### The impact

In sub-Saharan African BTV has been shown to be present in Ethiopia, Sudan, Kenya, Uganda, Tanzania, Botswana, Mozambique, Zimbabwe and South Africa. However, information is still lacking on BTV prevalence in other neighboring countries of eastern, central, and southern Africa. Past and recent studies have indicated the high level of antibodies to BTV in sentinel cattle in Western Kenya, reaching nearly 90% of cattle sampled being positive, indicating high exposure to the virus. Moreover, PCR positive cattle indicated that nearly 50% of them had an ongoing sub-clinical infection.

Fortunately, BTV does not infect humans and therefore does not pose a threat to food safety. But it does pose a threat to food security since sheep are one of the largest livestock population in sub-Saharan Africa, arriving only second to cattle, according to the Food and Agriculture Organization of the United Nations (FAO).

Understanding the dynamics behind what drives BTV spread can prevent new outbreaks. Several factors such as changes in climate can influence the spread of the virus. For example, rain and wind directions can significantly influence midges' distribution over large territories. The high prevalence and diversity of the BTV serotypes circulating in sub-Saharan Africa poses a high risk of introducing BTV to neighboring regions where BTV is controlled or absent, including Europe. A recent BT outbreak in Europe is believed to have originated from a serotype only detected in sub-Saharan Africa.

The only effective way to control the disease is through vaccination. Several vaccines are available for BTV, however, they are serotype specific. This poses a challenge as the vaccine will only protect against one serotype and will not provide immunity to the other circulating serotypes. Current research at partner institutions include developing multivalent vaccines that will protect against several serotypes at the same time.

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