P2 1: Molecular epidemiology of foot and mouth disease virus (FMDV) in Chad

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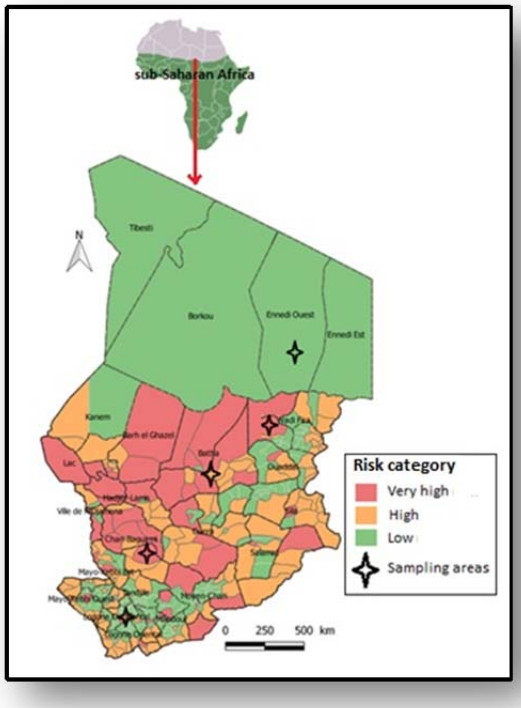

Figure 1: Risk of FMDV spread in Chad (based on data collected in 2016)

Foot and mouth disease (FMD) is a highly contagious viral disease affecting domestic and wild artiodactyl animals. Its causative agent is foot-and–mouth disease virus (FMDV: *Aphtovirus, Picornaviridae)*. Seven immunologically distinct serotypes (O, A, C, Asia1, SAT 1, SAT 2 and SAT 3) and many subtypes are described worldwide. FMD is one of the most economically devastating diseases of livestock. It is enzootic in many parts of the world including sub-Saharan Africa. Most studies on FMD are carried out in countries where control measures are implemented. On the other hand, in regions such as sub-Saharan Africa, where FMD is endemic and new strains are likely to spread due to animal movements, there are very few published studies on FMDV molecular epidemiology. In Chad particularly, no studies have been conducted to investigate circulating FMDV strains.

This work aims to understand the transmission process of FMDV in the pastoral area of Chad, based on a stratified sample of livestock herds (fig. 1). Susceptible animals (cattle, sheep, goats, and camels) were sampled according to the a priori risk of FMD spread in Chad, evaluated by a qualitative risk analysis combining the risks of its introduction and dissemination.

In total, 2,195 sera and eight epithelium samples were collected from October to December 2016 in six districts (Batha-Ouest, Batha-Est, Ennedi-Ouest, Wadi-fira, Chari and Lac Wey). Five out of the eight samples tested positive by real-time RT-PCR targeting the FMDV IRES region or the FMDV 3D polymerase coding region. Further analyses targeting specifically the VP1 coding region showed SAT2 type for four samples out of these five FMDV positive samples. Finally amplification and sequencing of the VP1 coding region of these four SAT2 positive samples was carried out to characterize more precisely the strains. Preliminary results were obtained for one sample, confirming the presence of a SAT2 virus, closely related to FMDV SAT2 viruses isolated in Egypt in 2012. Serological analyses are pending.

Filling the gap of knowledge concerning the FMDV strains circulating in Chad could both contribute to a better selection of vaccine strains but also to an update of the available molecular epidemiology data of FMD virus in sub-Saharan Africa in general.