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Zoonotic investigations of Zaire Ebolavirus in Likati, Democratic Republic of Congo, 2017

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Outbreaks of Zaire Ebola virus (EBOV) in people always start with a spillover event from wildlife. Which animal species constitute the reservoir is still not clear, but there is evidence for the involvement of several species of bat in EBOV ecology. In this study, we aimed to investigate EBOV presence among (small) mammals in the location where the index case of the 2017 EBOV outbreak lived (Kaigbono, Likati, Bas-Uele, Democratic Republic of Congo), 2.5 months after the start of that outbreak. The index case had been exposed to cooked meat of a dead Red river hog (*Potamochoerus porcus*) and grilled meat of a live captured fruit bat, likely a straw-colored fruit bat (*Eidolon helvum*).

A total trapping effort of 5460 terrestrial trap nights and 237 mist netting nights led to specimen collection of 241 rodents, 141 bats, 79 shrews, 5 monkeys and 1 mongoose as well as the molar pulp of the mentioned *P. porcus* remains, and we furthermore collected 97 environmental faeces/urine at a nearby *E. helvum* colony. None of the tested animals were positive for EBOV RNA in a qRT-PCR assay (including *P. porcus* molar pulp), and none of the 272 blood samples and 94 faeces were considered to harbor anti-ebolavirus antibodies on a 10-antigen Luminex assay. Notably, for only 91 individuals (mostly larger bats) was it possible to determine the specimen to the species level with certainty based on morphology only in the field. Sequencing mitochondrial genes for 332 animals revealed at least 47 species in our sample. Except for two species of rodent and two species of bat, most had low (1-20) per-

species sample sizes, indicating it had been easy to miss potential low prevalent EBOV RNA or antibodies in most species.

We conclude that more surveillance with large trapping efforts to reach sufficient per-species sample sizes is necessary to find the natural EBOV reservoir, and that genetic means to confirm small mammal hosts from this region at the species level are necessary.

(ORAL PRESENTATION)

Diversity of African mammarenaviruses and evolutionary relationships with their rodent hosts at various phylogenetic levels

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Mammarenaviruses are RNA viruses that are known to predominantly infect rodents, but some occasionally infect and cause haemorrhagic fever in humans. Like for other zoonotic viruses, it has been proposed that the tight evolutionary relationship between mammarenaviruses and their rodent hosts has determined their current diversity and distribution. On the other hand, also several host switches are known to have occurred during the evolutionary history of mammarenaviruses.

We screened a collection of 4151 dried blood samples from African small mammals, and genetically detect four novel mammarenaviruses from *Mastomys erythroleucus* in Ethiopia, *Arvicanthis neumanni* in Tanzania, *Praomys jacksoni* in the Democratic Republic of Congo and *P. jacksoni* from Kenya. We determine complete genomes of three of these, and of two additional previously partially described mammarenaviruses from *M. awashensis* and *Stenocephalemys albipes* in Ethiopia. With the presently extended dataset of 28 arenavirus taxa found in African rodents, we review African mammarenaviruses phylogeny and evaluate their host fidelity at various phylogenetic levels. We delineate five African mammarenavirus clades consistently at both genomic segments.

We confirmed the strong specificity of African mammarenaviruses for their hosts: most taxa have only been detected in a single rodent species or even a single intraspecific lineage, and eight taxa are circulating in sympatry in distinct hosts. While statistical association of mammarenavirus phylogenetic subclades and rodent genera is weak, on a deeper taxonomic