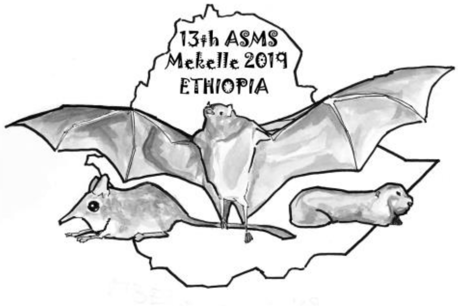

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molecular markers allowed to separate 21 "cryptic operational taxonomic units": e.g. *Scutisorex* sp1, (presumed to differ from *S. congicus*, *S. somereni*, *S. thory*), *C.* cf. *olivieri* is split into three distinct populations (*C. olivieri* sp1, *C. olivieri* sp2 and *C. olivieri* sp3) ; the clade *C. littoralis* contains three populations: *C. littoralis* sp1, *C. littoralis* sp2, and *C. littoralis* sp3., etc. Because of these cryptic species, the use of genetic tools, combined with morphological, cranio-dental, and ecological data, as well as the distribution areas in reference to type localities, proved to be usefull for reviewing the taxonomic status of shrews.

(POSTER)

An update on *Rhabdomys* sp. distribution, ecology and behavioural characteristics

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Until recently, the genus Rhabdomys was considered monospecific. Hence the bulk of studies addressing its ecology and behaviour reported population variations, which in light of recent knowledge could be species differences. Indeed, three studies described the phylogeography of the genus, revealing the existence of at least 5 species, occupying distinct environmental niches, although their distribution range and limits are still under investigation. Here we will, first, clarify the distribution of *Rhabdomys* species and, second, report on our ongoing research involving several contact areas between *Rhabdomys* species. Indeed, *Rhabdomys* offers the opportunity to address ecological divergence between species under common garden conditions, and we used this opportunity to investigate the impact of environmental conditions versus species interference on ecological and behavioural divergence within this genus.

(ORAL PRESENTATION)

Sampling distribution of bats (Chiroptera, Mammalia) in Protected Areas in the hinterland of the Kisangani region, DR Congo

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The "Centre de Surveillance de la Biodiversité (CSB/Kisangani) develops research Programs in the Protected Areas of the Kisangani region in order monitoring not only endemic, rare or endangered species but also their distribution in a perspective of pathogens transmission. The present research concerns the evolution of the sampling of the bats in 7 reserves because the human activities in human agglomerations and exploitation concessions (agricultural, mining, forestry, extraction of the building materials, ...) surrounding these Protected Areas greatly reduce the forested areas of these reserves and probably the possibility for the bats to properly rebuild its population once decimated, to shelter with tranquility or to get enough food energy.

For this, the bats were sampled from 2013 to 2018 using 3 mist nets (6, 9 and 12 meters) for 5 consecutive nights and identified with the keys of Hayman et al. (1966) and Rambaldini (2011). A total of 314 specimens were collected in 105 net nights with an overall success of 3.5 specimens per trap-night. The sampled specimens belong to at least 25 species. It appears from our study that 6 of 25 species are frequently collected in the Protected Areas (almost all the reserves), they are: *Casinycteris argynnis*, *Epomops franqueti*, *Hipposideros caffer*, *Megaloglossus woermanni*, *Myonycteris torquata* and *Scotonycteris zenkeri*. Monitoring of constantly sampled species: *Hipposideros gigas*, *Hipposideros ruber*, *Hypsignathus monstrosus* and *Rousettus aegyptiacus*. Species that are rarely or accidentally caught in mist nets are *Eidolon helvum* and Vespertilionidae (*Glauconycteris* sp, *Pipistrellus* sp, ...). Also, the Protected Areas around Kisangani City (Masako, Mbiye and Yoko) are the most diverse in bats (11 to 18 species collected) than those that are quite distant (Lomami and Fauna in Okapi).

(POSTER)

A new arenavirus in *Mastomys natalensis* mitochondrial matrilineage A-III in Ethiopia

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Mastomys natalensis, the Natal multimammate mouse, is one of the most widespread rodent species in Africa. It is the main reservoir of the Lassa arenavirus, highly pathogenic for humans in Western Africa. Six main mitochondrial matrilineages are recognised in this rodent species, forming two monophyletic clades A and B. So far, at least one arenavirus has been described for each of these matrilineages at the exception of the matrilineage A-III: Lassa virus in A-I, a Mobala-like virus in A-II, Gairo virus in B-IV, Morogoro virus in B-V and Mopeia and Luna virus in B-VI. We screened for arenavirus RNA presence 203 rodent, shrews and bats samples from Dhati-Welel National Park sampled in 2014 and found several positive *Mastomys natalensis* samples. We present preliminary results on the phylogenetic position and the genetic distance of this arenavirus in comparison with arenaviruses from other *M. natalensis* mitochondrial lineages.

(POSTER)