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**Editors:**

**BRYJA Josef, MEHERETU Yonas**

Parasitism is increasingly considered as an important potential factor affecting the response of species to global change. Parasites can regulate the abundance of their host population, influence the structure and composition of communities, and affect the composition of ecosystems.

In Senegal, rice production is still insufficient to cover household consumption needs despite the availability of arable land and a river in the North. As part of the national program of self-sufficiency in rice and large irrigation projects in the Senegal River Valley, agricultural development programs aimed at increasing production and stocks have been implemented. These changes are accompanied by an increase in the food resources and water around which human populations, livestock, rodents and associated parasites / pathogens concentrate and meet, with expected consequences in terms of health and food security.

It is in this context that our thesis will be implemented. falls in order to determine the rodent communities (identification of species) pests of culture present in the valley of the Senegal River. But also to characterize the species of parasites that they shelter (gastrointestinal helminths and dermatophytes fungi), and which could be source of diseases, but especially to impact the dynamics of these populations of rodents. This thesis will also make it possible to estimate the damage caused to the fields and the stocks by these rodents, so as to be able to alert but also to take adequate measures for a fight against these pests of cultures.

(ORAL PRESENTATION)

### **The phylogeny of the wood mouse (*Muridae, Hylomyscus*) based on complete mitochondrial genomes and five nuclear genes reveals cryptic diversity**

NICOLAS V. (1), FABRE P.-H. (2), DENYS C. (1), MISSOUP A.-D. (3), OLAYEMI A. (4), COLYN M. (5), BRYJA J. (6), VERHEYEN E. (7), KATUALA P.G.B. (8), DUDU A.M. (8), KERBIS-PETERHANS J. (9), DEMOS T. (9)

(1) Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles, Paris, France; (2) Institut des Sciences de l'Evolution, Université de Montpellier, Montpellier, France; (3) Zoology Unit, Laboratory of Biology and Physiology of Animal Organisms, Faculty of Science, University of Douala, Douala, Cameroon; (4) Natural History Museum, Obafemi Awolowo University, Ife, Nigeria; (5) Université de Rennes, CNRS, Station Biologique, Paimpont, France; (6) Institute of Vertebrate Biology of the Czech Academy of Sciences, Studenec, Czech Republic; (7) Royal Belgian Institute for Natural Sciences, Operational Direction Taxonomy and Phylogeny, Brussels, Belgium; (8) Animal Ecology and Resource Management, Laboratory (LEGERA), University of Kisangani, Kisangani, Democratic Republic of Congo; (9) Integrative Research Center, Field Museum of Natural History, Chicago, IL, USA

Woodmice of the genus *Hylomyscus* are small-sized rodents belonging to the family Muridae. They are geographically restricted to tropical Africa, where they are abundant in lowland and montane rainforests. Based on external and craniodental morphology, *Hylomyscus*

species were separated into six species groups: aeta, alleni, anelli, baeri, denniae and parvus. Within these species groups, *Hylomyscus* species are morphologically similar and, as a result, the taxonomy is still a subject of debate. We obtained genetic data (complete mitochondrial genome and five nuclear genes) from 141 *Hylomyscus* specimens, representing the six known species groups. This study is thus the most complete phylogeny of the genus to date both in term of geographical, taxonomic and genomic coverage. It confirms the monophyly of the genus and of the six previous species groups. Our species delimitation analyses suggest the presence of 24 candidate species in our dataset, 9 of which being cryptic, unrecognized species. Integrative species delimitation approaches including morphometrics, ecology, and distributional data are now needed to confirm their validity and to formally describe them. Diversification events within the genus occurred during the last 5.7 My and are linked to the evolutionary history and past connections among African forests. The first split is linked to the fragmentation of the African Miocene forest into the current Guineo-Congolese and East Africa forests at this time. The Early Pliocene marks a renewal of hotter and more humid climates, and possibly reconnected these forest blocks. The most intensive radiation of *Hylomyscus* is dated into the period 3.5-1.4 Mya and seems to be linked to several prolonged periods of strong wet-dry variability. The last period of diversification occurred during the period of climatic instability dated from 1.1 to 0.9 Mya.

(ORAL PRESENTATION)

**Population size and survival of the Malagasy fruit bat *Rousettus madagascariensis* (Pteropodidae) in Ankarana, northern Madagascar**

NOROALINTSEHENO LALARIVONAINA O.S. (1,2), RAJEMISON F.I. (1,2), RAMANANTSALAMA R.V. (1,2), ANDRIANARIMISA A. (1,3), GOODMAN S.M. (2,4)

(1) *Mention Zoologie et Biodiversité Animale, Domaine Sciences et Technologies, Université d'Antananarivo, Antananarivo, Madagascar*; (2) *Association Vahatra, Antananarivo, Madagascar*; (3) *Wildlife Conservation Society, Antananarivo, Madagascar*; (4) *Field Museum of Natural History, Chicago, USA*

Population size and survival are crucial factors to understand population dynamics of a given species, especially those that have long life spans and delayed sexual maturity, such as Pteropodidae bats. We studied the population size and apparent survival of individuals at a day roost site of an endemic cave-dwelling Malagasy fruit bat, *Rousettus madagascariensis*, in relation with age and sex. 1,801 individuals were captured and tagged over the course of four years in the Grotte des Chauves-souris, Réserve Spéciale at Ankarana, northern Madagascar. The Cormack-Jolly-Seber model and the POPAN model in the program MARK was used to analyze mark-recapture data and to estimate apparent individual survival and population size.